

901

TTTCCTTATT AATACTTCAG CTTCCCTAAC CTTCTACTTT TCAACTTAAG GGTACTTGCT	120
TGAGATGGTC TGAAACACTG TGTTTGAAAG CGAAGGCATC CAGAATTAAA TTTTAGTTAC	180
TTAAAAATTT ATTTCTCAA GTCTCTCTCA ATCTTGTCCTT ACATCCAGAA	240
ATGAGTAGTT TTCCAACAAT GGTACATCCA ATATCTGGAC TCCCTTTATT GTCTTTTATT	300
GGTTGCTAAC AATATGTGGA TGATTGCTTA TGCTCATCTA TTTTTTTAGA ATATTCAATT	360
ATnATTTAAA AGACAGAGGT GCAGAGAGGC AGAGGGCAGA GAGAAAGAGA AAAGGGGGGA	420
GGGTTCTTCA TCTGCTGGTn CACTCCCCAG ATGTCCGCAA TGGCCAGAGC GTGCCAATCC	480
GAAGCCAGGA GCCAGGATCT CTCGGGnCTC CCAAnGTTGAT GCAGAnGCCA AAGAACTGGG	540
GTAnCTTCTA CAGATTCCCTC AGGCCTAGAA GACAGCGGGGA TGAGAAAnTGG AGCAGCCGGG	600
ACTAGAACCA GCGCCCAAAT GGGGATTCTG GGCACTGCAG GCGGCAGCTT TACCTG	656

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

AGCTGAATCT TCAAATTACAC AGAAATTATG ACTTACAAAG TCATCACACA CTGAATTAGC	60
AAATACAGAG ACTCTGTCCC TAGTGGGAAT ACAGGATCAG GTGCCTATGA GCCTCTGGTC	120
AAAATATTCT CAAAAACAAT CAGCAAAGAT CCTGTCTAAA GAAACCTCAT TCAATATACT	180
GTGTTGCATC ACTGAACCTCA TAGCCAGTAG CTCCTTTTA AATTATTTTT TTAGATTTAT	240
TTATTTGAAA GTCAGAGTTA CAAAGAGAGA GGGAGACATA GAGATCTTCC ATCTGCCAGT	300
TCACTCCTCC AATAGCCACA ACAGCCAGGG TTGGGCCAGT CTGATGCCAG GAGCCTAGAA	360
CTCCATTCAA GCCTCCCACA TGGGTACAGG AGCCCAAGGA CTTGAGCCAT CCTCTGCTGC	420
CTCCCAGGTT CC	432

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TGATGCCTGC ATTATAATTAAATAATGCCT ATCACCGTTT CTTAAGCAAC AAATGATCAC	60
AGATTCCCTC TTTGCTGCTA AGTAATGAGC ATGGTGATTTC TTCCCTCCGT AACACACCTCC	120
CCACCTACAC TCCCTCCCCT CTTCCCTCCTT CCTCTCCTAT TGACATGGAG TGCCATACAT	180
AGCTAGGGTG AACATTTATC CCGCTTGGCC CTAGGTGTTCA ATACACTTCA ACTGTGTGTA	240
ATTATTCTATA TGCCCTTTT ATGACCAAGC TTATGTCAGA ACGACAAATT ATATATTACAC	300
CTAATACTGA GAATCATCAA ATTGATTCT ATTTCCTTCT CTCTTAGGCA GTTCTTGAGG	360
GGCAGAAATA TTTATTTTGT ATATCATGTA TTTATTCAAC TAAAAGACTG ACTGTCAAGA	420
TGCTGAGTTT TAGTGTCAAA GCAAATATGT TTCTAGACCC CATGAAGTTT ACAGTCTGGC	480
AAGAAAAGACC CATCTACCCC AAGAATATTG TTTAACATAG TAAATGCTGG TGTGAAGTCA	540
GTGGATAAAA ATTGAAGCAT TCTTAATCTA GC	572

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AAAAGGAATA AAAGAAAAAA CCAACACACA CACACACACA CACACACACA ACTGTTGAAG	60
GAAGCTCTCT TTGCTCTCAC TCTCACTGTG CCTTTCAAAT AGATGTGAGA AAAATGTGA	120
AAGAGGGAAA CAGAAAAGTA GGACACAGAG ATATGACACCG AGATGGACTG GACCTGCCAC	180
TGCTGTCTCT GAAGATGAAG GCAAGGGCCA TATGGTGGCA TCTCAAAGCT GGGAACTGCC	240
CTCAGCTGAC AGCCTATAGG AACACAGGAC TTGAAACGAA AACTGATTTT GGCACCTGTA	300
AGTTAATTAT TACTGTTAAC AACTACCTAA AAATATGAAG GGGCTGCATT GTGTGAAGCA	360
GGTAAAACCA CTGCTTGAGA TGCTGACACT TCATATAGGA GTGCTGGTTC AAGTCCCTGC	420
TACTCCACTT CCnATCTAAC ACCTTGCTAA TGCACCTGGG AAAGTAGTGG ATGATGGCTT	480
AAGAACTTGG GCCCCTGCAA CCCATGGAAG AGACCAGGAT GCnGTTCCAG TTTCTTGGCT	540
TTGTCCTGAC CCAGnCCAG CCATTGTGGC CAT	573

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs

903

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

CAGTTTGGA TAAGACAGCA ATGTGTTAAG CATATTCCCTT TGACTCAGCA GCACATTGCCA	60
CTCAATTTTC TCAACAGTTT GTGTAATAAT ACAATTATTG TTGTTATTAA TATTTTTATT	120
AAATTCCACC AATAAAATGCC TTAGTTGCAT CATCTTATTCTT CTTATTAAAA AGCTTTTTT	180
AAAAAAAAGTT TATTTATATT TATTTGAAAAA GCACAGAGAG AGAGAGACAG AGAGATATTC	240
CATCAGTTGA CTCACTCCTC AAATGCCTGC AACAGCTGGG GCTGGGCCAG GACAAAGCCA	300
GGAACCAGGA GTCAGGAAC TCATGTGGCA GAGACCCATG TCCTTGGGTG ATCATTAGCT	360
ACTTTCCAGT GTGCACTTTA ACAGGAAGTT GGATCAAAAG TAGAGCCAAG GTTGAGCCT	420
GGCACTTGAT CTGGGATACA GGTATCCCAG GCAGCGACTT GGACCACTCC TCCAAATGAC	480
CATACCCCAT TTGTACCAAC TCAGAGTGGT TCATGAATAG GCTGAAAGAG AGAACAGCTG	540
TTTAGTGCCT TACATATTTT CATCAAGGAA TACTTTTTT GGTCTCTTGG GATGAACATG	600
GAA	603

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

CAATGGGTnC AACCCAAGCC AGACCCCTGA AGGCCACTCA GAACAACAGG CTTGGGAGCC	60
AGTGTGTGG TACAGCAGGT TAAGCTGCCG CCTATGATGC CAGCATCCCA TGTGAGTCCC	120
TGTTCAAGTC CCGGTGCTCC ACGTCCAATT CAGCTGCCTG CTAATGCACA AAAGAAAGTA	180
GCAGCAGATG GTCCGTGTGC TTGGTCCCT GCACCCACAT GTGAGACCCA GACGGAGTTC	240
CAGGTTCCCTG GGTTCAACCC AGCCTAGCCT CAGCTAGGTA GCCATGTGGG GAAGTGAACC	300
AGTAGATGGA AACCAGCTCG CTCTCTGTCT TTCCCTTTCT CTAATTCTGT CTTTCAAAGA	360
AATAAACAAA CAAAATTGGA AAAACACCTC ACTGGACTGA TAGCACCTGA GTCCCTCCCT	420
CTGCAGCCCA TGCCCCAGTG TACACTCCTC AAGACACCGG CATGCACCTG CCTAGCCCCCT	480

904

CCACAAGGCA TTATCAGGGC CCCTCCCAGT GTTTCCCTCT CGATCCAAG GAGTCGAAGGG	540
ATTGAATCCC CAGGATTGn GCCGGCGCTG CGGCTCACTA GGnTAATCCT CCGCCTAnAG	600
GCCCCGGGGA AAAAn	614

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

CCAGACCGGA AGGAAGGAGT ACGAATGTTA TTGAGTGTGG AAACGATAGT GCAGATTTAC	60
TTCAAAATAC ACCAGCAGGG GCAGGTGCTG TGGTGCGGCCA GGTTAGGCCA CAGCTTGAGA	120
AACCCACATC CCGTATCAGA GTGCTGGTTC GGATCCCGGC TGCTCCAGCA TTCCCTGCTAC	180
TGCGCCTGGG AGGCAGCGGA TCAGGACCCA GGTACTCGGG TCCTGCCACC CACGTGGGAG	240
ACCCAGATGC AGCTCTTGGC TCCTGACGTA GCCTGGCCTA GTCCTTCTGT TACAGGCATT	300
TGAGAAACAA ACCAGCAGAT GGCAGATCTC TCTCTCTGGC CTCTCTCCCT CTCACTCTCT	360
CTGTTGTTCT GCCTTTCCAG TAAATAAATA AATCTTTAAA AAGATAAATA AAGTACCCCA	420
GTAAAAGCAA CCACATAACT TCTACACAGA AATGAGCAGA TGTATCAGGA CATTAAAGAA	480
AGCATAAAATG AATAGAAAAGA TGTA	504

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

TTTTTGAGAA CTTCTTAATG TTCTTATCAA TTTTTTGAGA TCTGCTCTT GCATTTCTTC	60
TATGTCATCA TCTTCATAAT CTTGAATTGG GGTGTCTTTT TCATTTGAGG GCGTCATGGT	120
GACTTCCTTG TTTTTATTAC CTCGGTTTT GCGTTTGTAA TTTGGCATAT TGGAGATATT	180
TGGTTTCTTC ACTGTGGTGC TTTTTCTTGT TATACTATGA CTCTAGATTA AGTGGACTAT	240
CTGTTTTGA TGGAGCCTTA GGGCTTGAGA TGGGTGTGGC CTGAGAGCTC TGTTGGTGT	300

905

GCCAAAGGTG ACACCTCCAG GTTACGGCGTG GTAAATCTCT CTCTCTCTCT CTTTTTTTTT	360
TTTGATTCAA AAGGGAAAGTA ATTCCGCACA GCTGAACGAA GTGGAGGTAG TTAG	414

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CTGATTTGAG TATTGGTCAT ATTCCTGAAA GACACAATCC TGAAAGCCAT CTACCCAAAC	60
ATTAGAACATC CAAAAGATCA AAATCTACTA TCTAAAGAAT CACAACCCGA AAATTAAAAAT	120
CCTTAATTTC GAAAACCTGA AAGCCAAAAT CCCCAAAACT TATTGCCTGT TTTTTTTTTT	180
TAAAGAGAAT CACTTTCTAA AACTTATTAA GTATTATTAA GAAAGGCAGA ATGACCAAGA	240
GAGAAGGAAA AACAGAGAGA ATGAGCTTCC ATCTGCTGGT TCACTTCTCA CATGGTCACA	300
ACAGGGAAAGG GCTGGGCCAA AGAAAGGAAC TCCATCCAAG TCTCCCACAT GGGTGGACAG	360
GGACCCAATT ACCTGGAATC ATPTCCTGGC TGGCCTTCCA GGTGGCATTA GCAGGAAACT	420
GGATAGGAAGG TGGAGTAGCT GAGACTCAAC CAGTGGCTCC GATATATGAT GGCGGTGTCA	480
CAGGGCAGCT TAACCTGCTG TACCACAAACA CCTGAACCAG TAAATGTCAT GTTTTTAAA	540
AAGTTATATA AGAGGAGCTA AGTCAAATCC GGGGATAGG	579

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CAGCTTATTT TGATGATTT TGATGGAGAC TACATTTAAG TCTGTAAAAT GTAAAAACGC	60
TTGTGTTCCCT TAAAGGACAT TTATTGTTCT CAAGATATGG TTAAAAACAC ACATTTAGGA	120
CTTGAGAACAT CCACAGTAGT CTGACATTTT ATTTCCACTC TAACACAATC ACCCGCCATG	180
CAGGCTCAGA ACTTTCTTTT TTGTGTTGT GGCAGCCTTC TCTCTCTCTC ATATATATTT	240
CCTCTCTCTC TCTCTCTCTC TTTnGnTCTC TCTCTCTCTC TCTCTTTAG AGAAAGAGTT	300

906

TATTGGGGAA ACCTGACAGG CTGGAGGGAA GGGGCAATGA ATGAAAAGAG GCAGTATGAA	360
AGCATTAGGG AGAGGCAGAG ACAGAGACAG AGGTCAAGGA GATGnGAGAT GTGGGATAGG	420
GATGGAGATG GTCCCGATGA GAGCAATGGA GACAGAAAGA GAGAGACATG TTCAGGAACA	480
GGTCCTTTTA AAACTTGCC CAGGGCAGG GGAGGGGAAG TAGGAACAGG GGAATCCCAT	540
TAGGAAGGGG GTGGAGCTTG ACACTGGTGG TTGGGCCATG TGG	583

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

TCnTAAGAAG GAAACTTTAA GCCTTGATA AATGAAAAAC AACCTCTTGT TCTCAGAGAT	60
AAATCATTAC AGTGAGAACT TTCTCTCCAA CTTTTAAAAA AAGCAGAATG CTAATCTTG	120
GCTTGCATG CTAGGGTTTC CCTACACTGC ACGCACTCCA GTTCTCTGCC ATTTTGGTGG	180
AGGAACAGCT CCTGTGGGTA AGTGATTTAC CTTCCAGCCC TTCCCCTGCG GGACCCCAAG	240
ATCTTTAACC ATTTAAGCAA TGGCATTTAA GTCTTAAGAA CCCCCAGAAG CATGCCCCCT	300
GGCTTTAGAC ATTCTCAAGT TTAAAAAAAAA AAAAAAAAAG GCCAGCTTGG GTATCAACAA	360
AGCAGAGAAA GAGTAAGCCA GATACTTCAG TTCTGATAAG GTTGGAGATC TGCAGCTCAG	420
GTAAGCTGAA CTGTAAACAA GACCCCTTCT TGCTTCTGCA GGGCCCTGGC TGCTGCACCC	480
ACG	483

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ATCCTACTAA ATTACCTTTG ATATACTTTT CAATTGACCT CTCTGCTTT TGTTTTCTT	60
ACCTTTGTGT AAATCCTCTT AGTTCATCCA AACCTTTTTC TGATTGCTCA GGTTCTCTTA	120
CTCCAATAAC TAGGGAAATC ATGTGGCTGG TAGTTCTTTC AACACACCCAC ACAAAAGAAT	180

907

GCTCAGTAAA TGCTTACTAA ATAATGAATG AAATGCCTTA CAAAGCTAGG GTGAACATT	240
AACCCGCTTG GCCATGAATG ATTTCTGTTT ATACATTTC AACCCTGTGTC ATTATTAATA	300
TGTCTCTTTT ATGATCAAAT TTATCTCTGA GCAACAAATT ATACAGTCAT CTAATTGTGG	360
CAGTTATCAA ATATATATCT ATTTCATTGT CTCTTCAACT AGGTAGTTCT GGGATCAGAA	420
ATGTATTTGT TTAATTTTAT AGCCTCATTA TTCATCAACT AAAAGAATGA CTATCAGGAT	480
GCTGAGTTTT AAGTCAAGCA AACAGTTCT GCC	513

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

TAAAGAAATC TTAAAAAATA TGCCAAAAGT TCACATAATC AGCTCTGGC AAGACAGGAA	60
GGTAGATAAA AAAATATGAG ATTATCATTG ATTTTAGAAA GGGATTGATG GTGTCAAAAG	120
TTAACTGTGG GGCGTGCAGT GTGAGACAGC AAAGTTAAAG CCACAGCCTA CAGTGCTGGC	180
ATCCCACGTG CACACTGATT CAAAGACTGG CTGCTCCACT TCTGATCCAG CTCCCTGCTA	240
AAGCACCCAG AAAAGCAGTG GAATATGGCC CAAGTCCTTG GCTCCCTGCA CCCATGTGAG	300
ATACCTGAAT GAAGCTCCCTG CATCATGGCT CCATGCTTCC AGCATGTAAA AAGAAACTAG	360
CTGAAGGCAG AACATGAGTC AAGATGTTAC AGGATTGGGG ATAATCTGAA AAGAGAAAGG	420
TAGTGTGATT CTGTATCCTT GCTTCCTCCT GCAGCTCTGA ATCTGTCATC AGGGATTAAT	480
CACACCTTAA CCATGTACAG CCATTCAGAG CCATGACATA TATTCTGGGA ACgtGCAGGG	540
GTCTGATCCA CCTGACTCAA GCAGCCCCCTT CTTACTAATA GGAGTTCTAC CAGTCTAATT	600
TTGGGCAGGG AAGGnA	616

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

908

TTTCTGTGTG TAnTTTTCA AATGAATAAA TAAATCTTTA AAAAAAAAAG GCAGCAGTCT	60
GCCATAATGG TGGATTATAC TTTGTAATCT ATCTGGAATT TGCTTGATA AAAGATATGA	120
AGTAGTGCTT TAACATTTT TTAACCTTTT TAAAGATTTT TTTTTATTTG AAAGACAAAG	180
TACAGAGAGA CAGAGAGACA AAGACCATCC ATCCACTAGT CTACTCCTCA AATGGCTGCA	240
ACAGTCAGGG CTGGCCCAGG CCAAAACCG AGTACTGGAA CTCCGGGCAC AGTCTCCCAC	300
GTGGGTGCAG GGCCACAAGC ACTTGGGACC ATCTGCCGCT GCTTTCTCAG GTTCATTAGG	360
GAGCTGGATT GGAAGTGGAA CAGTGAGGAC TCAACCTGGG CA	402

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GTCGGCAATGA TTAGACTAGG TGGGTCTTG CCACTGATGT GGGAGACCAAG ATAGAGTTCC	60
TGGATTCCCTG GATTTGGCCT GCACCAGCCC TGGCTGTTGT GTGCATCTGC AGAGTGAACC	120
AAAGGATGGG AGTTCTCTCC CTATTCTCT GTCTCTCTTT CAAAAAATAA AAATAAAAAAA	180
ATAAGAACAG AAAACCAATT GTGTGGATA AACCTGATT CCTCTCTTT CTATAACAAA	240
CACCAAGGAAG CAGGATCCAC TTCCCAGTTC CTTAAAAATG TGAATTCAAGC CAGTAATGGG	300
GCTATTGAAA CTTCTGAGAA TAATTAGATT GAACTTTCA TAAAGATAAT CAGAAAGTGG	360
AGGGAGAAGG GAGAACATA ATTGAAAGTA GTGACGAAAA ACACACAAGT GTCTTATAAA	420
ACAATAAAAT GTTTATGTTT TATTTTATA CCATCTTCC AGCAG	465

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GCTGTCTTCT GTTACTTTCT CAGGCACATT TGCAAGGAGC TGGATTGGAA GCTGGGCAGC	60
CAGGACTTGA ACTGACCTTC TGACATGGGA TGATGGAGTC ACAAGTGTGTT ACTGAACGTG	120

909

TTGTGCCACA ACACAGCACC CTTTGAGAT AAGTGTATAA TTTGCTTAGG TTTTACAAGT	180
ACTGGGTTAA GTCCATTGCC CGAGTAATAT GGCTAATAAT GGCAGAACCT CTCTGTCTAT	240
GGCCAAATGC CATGCATCAG TCACTTCCAC GTAGGCATAT GTTATCAGGA GTGGTCAAAC	300
GGCTACGTCG GTGAGCTTT TTCTTCCAAA ATAGGAAACT TTTGTGCTAA TCAGCAGAAA	360
GCACTGATTT AAGGAAGCAG TGATCTCTAT CAGCTCCAAA AGCATCTTCC ATAGATGTCC	420
ATTAGTTCA C	431

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

TGACCTTGCA CTCACTTGGG AGACCCGGAT GGAGTTCCAG GCTCCTGACT TGAGGCCCGC	60
CAGGCCTAGC TTCAGTGGTT GCGAGAATTG GGGGAGTGCA CGAGTGTGGA AGATCTTTCT	120
GTCTCTCTCT CTCTCTGCCA CTCTCTTCA AATAAAATAAA TAAATAAAATC TTAAAAAAAGG	180
AAAGAAAAAT GACTCCAAGT GCTGTGGTGG nAGGGGGGGG AAGGTCCCCA GCTGTATTTA	240
CTCCAGGTTTC TTATCTCCAT GTGAGATAAA ATTCAAAGTG GAGTCATATA TTGAATGCAA	300
AAATGAAAGG AGGATTATTAGAGAGAGA ACATTTGAAA GTTAAACATG GGTAGCTCTG	360
TGAGGAGAGG CACACACTAT AAGGAGCAGC ATTTGTAGCC CAGTCAGTG GTCTCTTTA	420
TTGGATAGGG GT	432

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CAAACAGAGT AAATTTACTT CTTTGATTCA CTATGATATT TTTGGAAGAC AATGAATTAA	60
AGACAACAGA ATGGGAAATG TTTACAATCT TCCAAAACAC GGCGCCATTT AATATCTATC	120
TAATTTTTCT AGAGTGAAAA GGAATCATAT AAATATTAAA TGGAACCCACA CGAAAGTGCC	180

910

AATATTTGAC TTTTTTACT GTTAAGGGAC AGGGTTTCAT ATGGCTCACT TTAATACATT	240
CAGAGAAAAT GTTAACAAGA AAACCCCTCTG AAGGCACGCA TCAGAAAACG CTGATCGGAC	300
GAAAGCAATT CTAGACTTGG CACCCCTTAAT GACTGCACAG TAATGGCCTG GTATTATAAA	360
GCCCCAAGCC CCACCTCTGTC ATAAAACATG ATTTCCCTTT TAATGTTCAT TACTTAGAGA	420
CACTGACAAA AAAATCTGAA GATAAATTAA AGCTCATAAA TACCATGnAC ACAACATACT	480
GTAGCAGAAA TAGATAATTG GCTTCACTAA ATTAAGTAAA TAACACAGAG TAGGCTATAC	540
CAAAGAATTG TGGCAAATTG TGGATA	566

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

TTCCATGGTA CAATTCATA TCATCTGCAA ATATGGATAT TTTGACTTCC TCTTTTCCAT	60
TTTGATGCC CCTTATTTAT TGTCCTCCC TAATTCACT TGTTGATTCT TTCACTTGTT	120
GATTAAGT GGGGAAAGTG AACATCCTTG CCTTATTCCA GATCAGAAGG GAAATGCTTT	180
CAGCTTCCC CATTCCATAT AATATTGGTC ATTGGTTTGT CATAATTAGC CTTTATAATT	240
CTGAGGTATT TTCTTTCAGT GCCTAGTTG TGGAAGTTTA TATTTTATCC ATGAAAATGT	300
nTAATCTTGT CCAATGGCTT TCTCACACTT ATTGAGATGA CCATACTCTT TTATTTCTTT	360
ATTAATTGGA GAAGTATGGA TTAGCTCTTC CAGAAATGTT TTCTAGAACATG ATnTGTAAATG	420
TCATTAGGTC CTGGACTTTT CCTTAATGGA AGACTTAATT ACTGCGTTAA TTTCATTGGC	480
CTGTnATGGG TTGGTTTGAG GGTGT	505

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AGAAGGGACT GCAGTGGGAT GGACCAAATC AGCACAGACA ACATCTCAA CAGTGCTTTG	60
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911

CnTnTAGTAG GGGTGAAAAT TGCCATTGAC TGATTAATGC TGTCTTGAGA ATACCGGATC	120
ACAGAATGCA AAGTCACTTG GGTTCTTCTG ATTCCTATGT GGATTGCAA TCATCTCTGA	180
GCTGCAGGAA AACTGAATTT CATTAAACAG TTCCCTACGC TGCAGCTTTC ACAGTAATTT	240
GAATGTTTCC AGTTATTTTT CAATAGAAAT TATTCTTTTC TCCGGGGACA AAACAGGCTT	300
CATCCTGTCT ATTTCTTGGC TGGTCTAAGA ATCTAGGTCA TATATCATTT GGAGATTTCA	360
CTCGGGCTAG AAGGGAAGGG ATAGTGGTTA GCTATTGCAA CAATCTCTAC CTGGACCATG	420
GAGGAACACT GGATTAAGCA CAATTCTTGT CTTTGGGAAG TATGGCATAA CCACACTTTA	480
AAGGGCAACA GACTCTCACG AGTTCCCTGGC ATTTTTCTC CATGTAAG	528

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

ATCTGAATC CCATTTGCTA GGCTGTAAAT GTCAATTCA CAATGAGTCA GCCCTCCATG	60
TCCACCTCCT GCTAAATCAG ACCTCCTCAT CTATTAATCC GTGGTAGAAA GCTCTCCCAG	120
CGTACTCCAG AGCTGGCTAT GAACTGATAC CCGCACCGTT TGGCTTCCAG AATTGCAGGA	180
CTCCAGAGTG CAAGACTTAG GCAGACACAG TCATTGTCAG AGCCTTGAAA GGAAGTGACA	240
GCCAGACGGA GGAGGAGTCA CAGCAGAAGT GGTCAATCATT GCTAGTACCA AGGCTCCTGT	300
CTGAACCCTG CCTGCCATGT CACTAGCAA AGATGTGAGG ATCAGTCTCC TATTTTTAGA	360
ATCTCAGCAT CGCATCGTGT TGAGGAATTG GCAGGCTAAA CTACTAGCCA AGCTGGGATT	420
CCTCCTGGAT GTCCCTGGAT CATGCTATCA GACTTGTCCCT TTCTCCCTCC CTCTCCCTCC	480
AGCCTACATT TCAGCACACT CCTGTTCTAC CCTGGCTGTT CCATACTCCT CTAATCTAGT	540
CTGCTCTTT TCTCTGTCCA T	561

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

ACGTCGTGGA GCACnTGGTT GTCAAGGTTT CCTCACTTGG GGTTTCTTC GTCATTCAT	60
CAACGTGTGC TGGTCCTAGG AGAGACAATT GGAAGTGTGT GCTCTCCAAT CGGTGGGTGA	120
GAGCAGTGTC ATCTTCGCAG GCTGATGAAC CACCTGGACC AGGCAAAGCC TGAACGGAAG	180
AAAATGGGGG CGATGCCAGC CAAGCCCATT TCTAAGTCAG CCTCTTCTGA ACCAACGACT	240
CTGGCTCCTT CCTTCCTCTT TTCCCTCCTCC CTCTTGCATC CTCTTCCCC ATCCCTTCTT	300
ATTTTTTGCC TCCTCTCTGT CCTCCGGTTC TTTATTCCT TCTCTCTTG TTTGTCTCCC	360
TTATTCTTGG ATTCTTTGTT CCTTTGTGG CAAGGCAGAA CTAAAATAAG GTAGTTCTCA	420
AAATTTCTGT TTTTGGGGAT TTGTCCAAG GCGTAATAAA AATAAGCACA TTAACTTGTG	480
ATATCAGATC GGAAGTCTAA TACATGAGCT GGGTTGAAG TTTG	524

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

TAGCATTCTA CCCAGACACC CTTGCTTTTC TGCCAGACAT AATCTACATG AATCAATCCC	60
AGGTCTTCCA ATACAATGTA GCTTGCTACT TCAGGAGCTG GATGGTGTAC AATTGTTCAC	120
AGATGCTCCT AATTGCACCT GGATCCAATA ATAACCAAAT ATTGTTAAA GTTTGGCAG	180
CAACTATTTTC AGGAGATATG TAGGATGAAT GTTGAAAGT AACACTCCAG GCATAAACCT	240
GCATGAATTA GAACCTGTAG GAAACATAAA CACAATTCAAG TAGGTGGCAC TATTCCCCA	300
GTCAGAACCT TCTTCATTCT GCATGACTTG GCAATGACCT TTATTAATT ATTCCATGGA	360
ATTCTGTGAC CTCAATTGAT ACCAATATAC TCCAAATACA TATTCTGGAT TCTTTGAGAT	420
ACCACAGCCC AGGTAAGAAA CAATCTATAG TAGCAGGTAT AAAAATACAA AATCATTGGT	480
TTCATCTGAA GTCCTAAGGT AATCAGATCA GCAGGTTACT TGAAGTTAAT TAATTCCAT	540
CCCCATCAAA CAACCCAAATT GGA	563

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

ATTTCAGCTC TCATATCTTA CTTCTCAAC	TTTAGCTAGA TTCCAAAAGA ACTACTCTTA	60
TTGGCAACAA AAAGAACTAT AATTCCATTG ACAGAAACTC CATGTTAGAA ATGTATTCAA		120
TCCAATCCCC ATTACTAAAA TAACATGTTT CATTATTTT GTTCCATTAA CTTTAATAAT		180
TGTGTAAGAA TTAAAAATCC TATGTCACTC AGAAAACCTCA TATTCACCC TTAAAATGGC		240
CATTCTAAA TGGACTAATT AAAAATTTA AAAAATTAAC TCCTCAACTT TAGAACATTG		300
GAAAATGAAG AATATGTCTT CTGGGAATT AGAAATTGTT ATTGCAATCT TATTAATCCC		360
CTTATTTTTT GAGTGTATAA TGTGCTACA GTCATCTAAT CCACACTAAT CAATCAAAAA		420
GCTTTTATTA CTGAATGTTG CAGTGTTCAG CAATGTCCTA GACACTGGCA GGCTTAAAAA		480
TTCTAGATTA AGGCCGGCGC CGCGGCTCAC TAGGCTA		517

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CATTGCTAAA CCTTAATCAT GGTATCATTC AAATAGTAAT TTCTTAGTCT TTCACTTGGC	60
CCTTCCTTTT GTTTTACATT AACGGTTTTT GTCTCTCTCT CTCTCTTTTT TTTTTTTTTA	120
ATAATCCATG CGCCCCAATT AAGTCCAACA TCGCTGATTT GGGGCAATAC AGAATCCACT	180
GCACCATCTA ATCTGAGTAT AATTAATCAC TGCAATTGCG ATACCAATGC CCAATCTGTA	240
CCCACAATCT TCCTCCCCCTA AACTGTCGCT CCTGCTGGAT GCTCTCTAGA CACACCACTG	300
GCCCTCACCT GATATTCCAC ATCCCCTCCT GTCTGGCAAC CCCGAAATCA AACTTTCTCA	360
TCTCCATTGG AAAAGTAATT GCTCTTAGTA ATTAATCTTG TTATTTCTT GCTAAATAC	420
TTGAGTGAAT TCCAAGAATG TATAAGTAAA ATTCAATTTC CATAATACTG TACTnTA	477

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

TGTAAAGTTT AGGACAGTAA GTGTAAAGTC ATCCCTGGAG GATAAAGTTG AGTTTCTGTA	60
TTTGCTCAG GAGACAGCCG TGTACCCCCG GAAGGTCACA GCCTCTGTAT TCCTGTGTGG	120
TAGAGGTTCT GCTGTTGTG GACACTTGAG CTACTTTCC CAGCAAACGG AGCAGGACAT	180
AAAACCTTTC CCCTTCTGG GTTGTGTAGG CAGAACAGA TGGCTAAAGA ACATCTTAAG	240
ATTAGACACA GGAAAATGCA GGTCCCCTG AATAGAAAGG AGTCAGTCCA TGCTGCTAAA	300
TGAGGCATCC AGGCATTTG TAGAGCATAA CAGAGAGGAA GAAACCTAGG TTAATAGTTA	360
CTTGATTAA AATGAAACTG TCCCTAAGGC GGCTTGAAA TGAGACGGAA GAAGGACTAT	420
GACACCAGAA TGTATGTTCC CAGCACAGAA TAGTGTGAGC TGAGGGACAT GGCAAGCAAGT	480
GCCGAGGCTC AGAACACAGA GATTCTCCTT GCTGTAGTCT AGAGCAGGGA TCTCATCAGC	540
TTCTCATCAG GTACAAATTG GAAAGAAACA CAACTTACTT TATATATATn AGCCnCATAT	600
ATATGTGTAT ACACACACAC ACACACACTG AGGGCTGAAA TTAATGC	647

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AAAAAGAAGA GTATTCAATG GGACTGGGCC CCCAGGTAAT CACAGCAGTA ACCAGCTCAA	60
TCATACTCCC TTGGGTTGCA CTTTCTTCTT TCCATTCTAC ACTTTTCATT GTCTCACTAT	120
TGTCCCCCTG CCTTCCCTTG CCAAAATAAA CTCAAAACTC AGAAAATATT AAGAGCTTAT	180
CTTAGAGTGT ATGCAACTTT GAGTGTCCA TTAGATGTCC AAGTGGAGAT GGCAAGGAGG	240
CAAGATGACC TAGAGTCTGG AATTGAACAC ATAATGTGCA GAAGAGACCA GGTTGCTTGT	300
CTTCAAAGAT CACTGTTAA GGATGTGTCA GACACTCCC CCTTCAGAGC CTCCCCCGAT	360
ACAATGCATC TCCATCTCCT GTTGCTTGG TGAACACTCC TTTCTGGTTC TCAAGAGGAG	420
CCAAAGAAGA GGCCATGCTC ATGGAAGGCA CAAAAACCTG TCCTGCCATT CTGATGATT	479

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GGTCTAGTTC CAATATGGGC ATTTGAGGAA CTGCATCAGA TCAGAGGAGG ACATTTTACA	60
GGGCAGGAGG GCCTTTTGCA GCAATGTGGA CACTACAGAT ACTATCTGGT AGAACATGCTCA	120
GGAGAACATGGG CTCTGTGTGC CATATACCAT TTGAAACCCC TGCTGAAACC TTTCAAGTTGT	180
GGAACATTTC TTTCATTTTA GGTAGAATAT GTAGAATTAA AAGTGTCAAA AATCCACTGA	240
TGAAGAAAAT GTTATTCAAC TTTTCCCCTT CCTGTTTCTT GTTTTCCCCCT TCATGCTTCT	300
CATGAACAGT GGTCTCAGCA TTTCTGTATG GAAAACCTAG AGAGTTTCC AGTGTAAAAA	360
CTTCTAACCGG TCTCAAGTGA AATTCAGGG ATATATTATC AAAGTGCAGG TTGGTTGGCA	420
TGTACTTTCT TGGCATGTCT TAAAGATAAT ACAATTCTAA CGGACAGTCT TCCAACCTAA	480
GGGATGGATA TGTAAGTTTC TCATCCCTAG GGCAAGATGG CTTATCTCTC AAGCCAACCTC	540
CCAGTGGATT TTTGGTTATT TTTTGTGnTT CTGTTGTGAA CTGTGAAGTC ATTGCTACCT	600
CTGTAGGAAA GAGGACCGTG AGTGGCTAnG TAGGGTCAGC TGGAGA	646

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

ATAGAATTGA GTACAACTTA AGCATGTGAA CTCTGAAAAA AGACTTGCCT AGGTCAAAT	60
TGTAACCTCTT CCATTTACTG GGCATGGGAT CTTTGGCAAG CTACCTGAGT GTAATGGGCC	120
TTCATCTGCC CCTCTGTCAA TAGGAGAAAA TAATGGTGCC AATTTAATGA ACAGCTATGG	180
TTGTTAAATG AAATGATGCA CATAAACACAG CTCACAATAT GAACCTCGTG AGTGATTATT	240
CATTATTATT ATTTCCAAAG AAAACTTAAC AAGTTAATGG GACCAAATAC TTCTGTCTGG	300
GGTGCAGGTG GGGGCAAAAT ATCTAAATTC TGATTTTAGG AGAATTGAT CCAAAGTTTT	360
ATAGTTTCCT GTTTTAAGT CCTTGGTGCC ACTGTCTCCT CTGGTACAAA TTCAAGTGAT	420

916

CATGTCACCT CCCAAGAAAAC TTCCCTGCTGG AAAAAAAAATG TTTTCTAGGG GAAGAA

476

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

TGCCCCnATC ACGCATCCGC TCAAAGAAAA GCACATACCG AATACACCGC TCCCCCGCCA	60
ATTGCTGCAC CGCAAGTGCC ACACCAATTAA TTAGCAAGAG AGTCCAACAC ACCGCCCTCA	120
CTACACCGTA CAATGCTGCC CCATCCCTA TCATAAGGGT CCGGTAATC CCCCCGAACC	180
TTCAAAATAC GTGATAAAAG AAACAAGCCC ATTGTAGATT CCCTGCGCGC ACCTTTCAA	240
GTAGTCCGCA TCGTTGAGCA ACCGCGCCTC TACCGGATTA CTCACAAAGC CTAATTCCAC	300
CAAAACACTT GGCATCTTCG CGTCCGTAC TACAAACCAG GCCTCCTCTT TTACTCCACG	360
ATTTTTACTT TGTGCACCGA CGCTTGCTTG CATTCCGTCA GCGATACTGC GCGCAATCAT	420
AATACTTTCC ATTGTGAATT CCTCTTCGAG CATCGAGTTC AAGATCGGGA GCACCT	476

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CTTACTCACC ATCCCTTGAA GGGCAGGCGA GGGATTGGAA AGGGGGGAGA AACAGGCAGG	60
GAGCAAAGGA GGCAGTGCAT ACTGTTGAAG ACTGGAAGGT GTACACAGAC ATAGAGGCTG	120
CATGGAAAGT CCATAGGAAT AAAGGAAAAC CCCAATCATT GGCTTACAGA AACGGGCAAA	180
AGGGACAATG TGCAAAGACA GACAAGTCCC TGTCACTTTT CTTCTGAGAC TCAGGAGAAC	240
GCCTGAAGCC CAACACATGT ATACATTGTT TCATATTCA GTGAGAGAGA ATATTAATAG	300
TACCCATTAA CCAAGTACCT TCTGGATGCC ATCTGATCCT TATGGTCAGT GTTACCATCT	360
CATCTTACTC AGAGGACTCT GAGGCTCAGA AAGTTAAATA ACTGTCTAGA GTCACACAGC	420
TGTAnGGACA AAGCCCCATAT CTATACTCAG TCCATCTTCC AGTTTATTTTC TCTGGCTGTC	480

CACTAGCATC TATTTCTAAA ACAGCAA

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

AACCACTACT GTATATTATA AAATCAAACC AAACTGATAC ATAGTTATCT GTTGCTATCC	60
AAACCTATTT GGCACCCAAG TTTGCACAGC AAAGGCTGGT AAGGGGTATG CATTCCCTCAA	120
GGCTTTTGA TTCCTGAATT TTGAACAGCA AGTGGTGAGA GTTTTGGAAA GCAAGAAATT	180
CACAATTCCCT TTGTTACCTA ATTTGCACT GGAAGCGTTC TGGTAGTGAG GTAGCTAAA	240
TTGCAGTTTT GAGGCTGCAC TTGGATGCCT CATTATGAC AATTACTTAA AGTGATTAGA	300
CTGGGTGCCA GGAAAGGAAC TGAGCATTAA TGTGTGCTCT TTCCCTTGGT CCCCCATAGGA	360
ATCTAGTTAG GCACCTGTCT TTGTTATCTA GATGAGGAAA GTAAAGGAGA GGTATGCTGA	420
CTTGCCTCAG TCACAAAGTT AGTGCCAGAT GGAGCCAATT CACCGACACA AATATGTGAC	480
TCCAAAGCCC ATGGATCGGT TTGTCATC TC	512

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

AAGATTGTCT AACTGTGCGC ACGTCTGAGG CATTGTGAGG GTAATGCCA CGGGTCTGTC	60
CCACCTGAGG ATCCTCCCTC ACCGCCCCTC CCACCTACGC CTCCCCCC CA CGCCGGGGC	120
TGATGGCAGC TTCCCTCCCTT CCAAGCAGTA ACGACTCTGC CCTTTTGTGT TAGCCACATC	180
TTTAATTTC TTTCTATTTT TGGCACCCAA GTATCTCTCC AAATAATATA ATTAAATTTC	240
GTTCTGAAC GTGAAATACG TGAGATCATC CAGGATTGCG TTGTGGAGTT TGCCACGAAA	300
GGAATAAGCT CAGCTATAGG CAGTGTCCCT CACTCCTGAC TCTGCAGCGG CCGTTGGTGG	360
AGGCTGGTGC GTGTGCCCGG CGGGCCAGAG CCTCTCCACA GGGCACCACC TTTCCCCGCG	420

918

TGGCCGTTTC AGCTCTGCCCGC TGCAGTCCGT CTGTGGTCCG CATTGTCCGA GGTGACCGGT	480
CATCGTGGTT TACGTCGCA	499

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CTGCATAAAA CTGCTGCTCT GAAGTATCTT GCAAGACAAA TGCTTTACA AAATTTGCAC	60
CTACACATAA TTAATTTGGA TAAATTATGA AAAAATGGTT TCATGGAGGG GAAATAAGTC	120
ATTCTACTT TGATTTGTG TATCTCTAT GAACCCCATA ATTGTCTCAA TTTACTGTAC	180
TAATTTCTC TTTGCCCACT CTTCAGGTTT TCTTTGCTT TCATTTCAGA CTTAAGGTTT	240
ATGACATTTT CAGCACCAACC AAGGTTTGAC CAGAGTTCTT GTAATAAGAA AAATCAACAG	300
CTGTGATGTA CATACTATT TGATTACATC TATGTCCAA TTTTATTTTA AGAATTGTGT	360
TTGTTATTAA CAAAATAAAC TCGCAGGAAT GATGTCTGCT TATATGATTG ATTAGTTCA	420
GTCCTAAAAT TATAAAGAAT GTGTTAAAAA ATAAAGATGT TTTATGAAGC TCTTTCTTCA	480
TTTGAAGAAG CAGGATTTT CCTCCAGGTC TCAGTATTTC ATTGTGG	527

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

ATTATTATAA TTAGTATCCC ACTTAATAGG TTCCAAAATT CCTACTTTTT AATTAAATAT	60
ATAAAAGTGAT CTGCATAATA TAGAAGTTTC AAATCCATTCTCTAAATTA AAAGTCCAAG	120
TTGAAAATC GGGTTTGGTT AAAAGCTGTG GAAGGAGAGA AATAAAATAA AAACCGTTAA	180
GAGTTAGCTT TTATTGAGTG ATGGATTAG AATGATTTC TTCCCTGTG CTTTTCTGCT	240
TGTCAAATTT CTCTAAAATG AGTACTAAAA ATGTAAACAC AAACAATTAA AAAAGCTGTA	300
TGTCAGAAAT GTGAATGCTT AAGTAAGCTT TTAATGTTAA AAAATAAATA AATAAAAGTCT	360

919

GAATTATACT ACTCCAGATG GCTTCAGCTG TGATTCGTGC ATAGCATTG AAAGATCGTT	420
TTTTTACATA AAATACCCAT AACGCTAATG TACTAACACCG GAGGTCCACC GGACTCCCAC	480
TGGGTTTCTG AAGGGAATGA AATCTAAGCC GTTAA	515

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GGTTGGTGA GGTTATTGAG TGTGGATGG GTGTAGGTGG GGTTGGAGG GATGGTTAGA	60
GGTATAGGAA GAGTTAGAG GGGGGnTGAG TGTATATGAT GAAGGGGGGG GTTTTATGAT	120
GTTGAGTGTGTT GATATATATT AGGTAGGGTT AnTTAGGGG	159

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

AGCACTTGCG CGCAACCTG CAGCTTGCCTG nTCAGTCCCC CGGCTCGGCT TCCGCGGCTC	60
GGCTTCCGCG GCTCGGTCCC GCGGCTCGGT CCTGCGGCTA GGCTTCGCG CGCGGTGGGC	120
GACCTTGTTC TCCCAGTAGG TCCTCCGATT TACGCCACT GGATCCAGAA GAGTTTCGTC	180
TGCAATATTT TCCTGGTTCT TTTTTCTGAG GCTACCGTAA CTCCCCTTTT ATTAAACTAA	240
ATTTTCCCGG ACTATCGGTG CGCGCCCTCA CTATTCCGCC ATCTTGGCTC CGCCCCCCCAG	300
TAGTTTTTTT TAAGGTTTTT ATTTTTTATT GATTTGAAAG ACAGAGTTAC AGAGAGAGGT	360
AGAGA	365

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

AAAGAAGAAA ACACGTGAAA TAATGTTGAT GAGCTCCAGC TACTGGTAAA GATCTTAGGC	60
TTGACCAAAAT GTGATTGCT GTGTTTCCTG TTTTGCTTCA TTCATGCTGC TGTAACAAAG	120
GACTAAGATT GGGGGGTTTA TAAACAACAG AAGTTTCACT GTTTTGAAAG TCTCAGGTCA	180
GGTTGCCAGC AGGGCCGGGT TCTGGTGAGA GCTGTCTTCT TGACTGCTAA CTTCTTAATG	240
TGCCCTCACA TGGTAGAAAG AGCACTGAAG AGCTCCCTGG AGATTGTGTT TTAAGGGCAC	300
TAATCCCGTT CTTGAGGACT GTACCCTCAT TAGCCAGTAA CCTTCCAAAG GTACCACACC	360
AAAATATGTA TGA	373

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

GCTAAAATCT CACATTTTT TTTCTTTTGT TTAAAGGGAA ATCCTCACAT TCACCTGATA	60
CTCAGATGAA TGTGAAAGTT AAAATCTTC TCATTCAAAA GAGCACACAG CACAGATTGA	120
GTAAGAATGA AAATGCCTGT GGAGACACTT CTGGGTGGTC CACATTGTAT ATTGCCTGTA	180
AGTTTCACTC TTTTCTTGTC AAAGACTTGA GATTCCATTG TAAAAATAAA TCAACTCAGT	240
TGGGTAAAC AGTCCAAAGA AAACAAAAAA TTTATTATCA AAATAATAAT CTAGGCCTTG	300
AATATTTCTT TCTCAGACTG AACTGAGATA TTTCTAGAAT CAAAGCAGAT GTCACCCATC	360
CTGACTAAC TACACTATTT GCTCTGGACT TATATGAGAT TTTTCCATTG GTGGCTGCAA	420
TTTCCAATCT CAGTGTAAAA TTACTTCGGA TAAAGACAAC AATT	464

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

921

TCATTTTAT TAATCAGCTC CGCATGAAAA TAGGGATTAT GTTTGGGAAT CCTGAGACTA	60
CTACnGGnGG CATTGCAC TT AAGTTTATT CCTCCGTGAG ATAGAGGTTA GGAAGGTGGA	120
AACGCTTCAGAGGTGATG AGGAAGCGTG GGGCAATAAG GTAAGGATCC GGATAGTAAA	180
GAATAAGATG GCACCCCCCT TCCGCAAGTA GAAACGGAGA TTCTCTTGG GAAGGGTTTT	240
TCTGCCCTTT CGTGTTGCT GGATGCAGCG GTTAAGCAGG AAATTATCGA AAAAAAAGGG	300
GCGTGGTACG CGTACCGAGA AGAAAAGATC GGACAGGGGC GTGACAATGC CGTGGGCTTT	360
CTGCAGCAGA ATATGGACAT CACCTTGGAG ATCGAACGGG CAGTGCCTAC GAAGCTTTTT	420
CCTAACGCAGG CGTTTATATC CAGCTTCAG GAACATCGTC CTGCTC	466

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGATACTGG GGAGCGGTGT GCGGAAATTT TTGTGTGGAC CGCGCGTATG TCCGCTGTAC	60
CGGGCCGTGT GGTTACCGTT TGTGTACGTG GGTGCCGTGG GGAGTGTGAG TAGCGTGTGG	120
AATATCTCGG ATGCCTCAA TGGACTGATG GCGTTGCCGA ACCTGGTGGG GCTGTTATTT	180
TTGGCTCGTC A	191

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

CATGTAACTC TGCCCTCAA ATAATAAAAT AAATATTTAA AAAAAGAAA ATGTACATTA	60
ATATAAAACA ACTTACAATC TACACCTAAT TTGTTGATGG TAAATAGGCA ATCTTCAAAT	120
TTTCAAATT TCCAGTTGTG AATTGTCTG CTTGCTGAAC TCTATTGCA ACTCCAAACT	180
CAGTGCTCAC AACACTCACA GGCACACGGA GAGTAGGAAA AAAAAGGC AAAATTCAGT	240
CGCAGAGGAG GCTGCACGAG GCCACACTCG GTCTCCTGAC GTTACAGCCG CGTCCTTCGG	300

922

GGGTCTCTGT GTGCTGTCGC TGGTGATCCA ATTGTTGCAA CCAGTGTCC TGCTCTGTTG	360
CACACAGGGC TGTGGTCTCA CAGTCGGGTG TGGTCACAAG GTCTCCTTGG ACAGACACAC	420
GTCCAGCCAG GGCGCACAGC GGCGCAGACC TGACAAAGCC GTGTGTGCAG TGACTTGATA	480
AGCGTAACTC CCGCCACCCGG CAAGAACTGA GAATTGAAGG GAGACAGACT GGAGAGACCA	540
ACAGGGAGCT GACCGAACGA GTGATATCCT CCATGCCAGA GCAAACGGAA GAGGACAAAG	600
CACAGGCCAG ACCGCCTTGT CCTAAnTGGG G	631

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

CGCAGCGCGG GnCGAAGGCA CAGTGAGAGG TTTCAGACAC GGATGCGCCG TGTGACGTCC	60
GCTGGGGAGC TGAAACATCG CGAATCCGTT CCTCCAGCGT TTTTAGGGGA ACACGACAGG	120
GCGTGGTGCC TGCCCCTACG TCCCCAAGCT GTGCCGCTGA GGTCAGGACT TCTTTCTCCG	180
GCTCTCGCGC ACCGGAGCAG CTGGGGACCG CCTGTCCCAG GCCTCCCTCC CCGCTGCTCT	240
CCCCAGCCCG GTCCGAGGAC TGACCTCCCA CCGGTGAGTG AGGGCGGTCA GGCGGGGCTC	300
GTCTCTCTGG GTCTCGCTCC TAACACAGCG ACAACCTCTT AGGGGAAGAA ACCCCTCTTG	360
TCAGGGTTCA GTGAGACTGG GGACCCCCAA TCCCCCAGAC CCCCGGTGCT TGCAGCCCAG	420
CCGTGGGCCCC TGCAGATCCG CGGGACAnGC ACGTCCACAG TGCTTCTTTT CCGGAAATGC	480
TCCCTTCTGA GCCAGTGCTT CTGGTACAGT CAGAAT	516

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ACTGTGCCAG AGCGCCGGCC CCCGAGTGGG TTCTGATTAA GATGTTGAG GACCACAGTT	60
GGCCTTCCCT CTTGATGAGA GCCCAGAAAT TTCCCAAGTGA GAGGGGTGTG GACTTAGGAG	120

923

ACACCCGTGAA	GTCCGGTGGC	CTTGGTACT	TTGTCAGCGT	CCGTGGTACT	CAGCCGCTGA	180
GTCAGGACAC	CCGGGATTGC	TCCTACAGAG	CTTGGATTTT	CTTCCGGCT	GAGCACGTCG	240
GGACCATCAA	AGCCAGCATC	TCAGCCGTGG	GTGCGTGGGC	AGCGGCTCTG	AGCAGATGAG	300
GCTCAGGTGG	ATGGGTTCCCT	CTTCTGCCA	GGGAAAATGC	CTCAGGACCA	CTTCTCTGCT	360
CTCCTGGGAC	AGGAAGGCCA	CAGGCTCATT	GCGATTTTTA	CGGACAGCAA	GTCATCCTGT	420
CCGTTGGCTG	GGAGGACTCC	ATCTTCATAA	TTCTGGAGTC	CTGAGCTTGA	CGTGAUTGCA	480
GCCATTTGG	ATGCACTTGC	TGTGTTGCC	TTGAGTAAC	CTGAGGTCC	CCCC	534

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

TGTATGTGCA	TACGTGCTTT	CCCCCTCTGT	TGAATGCCTT	CTCCTCTGG	TGAGCTTTAC	60
CTGCACAGCC	TTCTCCTTCA	GGGCCATCAG	CTGCGCGTGG	CTGAAACCCCT	GGACAGCCCC	120
CAGCAGCTCC	ACGCTCCTGA	TGAAAGTGTC	TCCGTCCATG	CAGAGCAAGT	CCTCAGGGGC	180
CCAGCAGGCG	TTGGCCTCGG	CCAGCCTGAA	GATGTCATTG	GGAGAGGGAG	CCACGACTCC	240
ATGGCAACCT	GAAAAGTGA	TGGGAGACG	CAGGAGGGGA	CGGGGGAAAGC	AGAAACTCAGG	300
GCAGGTTAGC	CCGATTCTCT	CCTGGAATGA	GGAATAACTC	ACCCCAGTCA	GATTATTCA	360
CAAGATGCCT	TTCTTGCTGG	TGACCAGCTA	CTAAAATGGT	GATACCAGCT	TCTTGCACAT	420
CCACATTGCC	ACTGGACCAC	ACAAGCCAGT	GCAGTGAGAG	CTGGTGGTGG	ATACTCCTGA	480
CATGAGATTC	AAACCCAAAG	CCACTnGnC				509

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

TTATGATAGG	ATTGTCATAA	AATCATTAAA	TAAATTATTT	ACCCATTCA	GCAGTGTGAT	60
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924

TGGCTCTTGT GCATTAGATA ATATGAATGG AAGGGAAGAC TGT	120
TTTTAACTTT TTTTTTATTT AGGGTAAACA AATTCATGT AATTCA	180
AGAATATAGT GCTATTnCCC ACCCTACCC CCACTCAGCC CACAGTC	240
TCCTTCCTCT CTTATTTCA CTCTTAATTT TTATAATGAT CTACTTT	300
ATTAACCCTA TATAAAATGA GTTCAACAAA TAGTAGGAAT TAAAAAAC	360
CAGTAGAGAC AAGGGCTGTA AACAAATCATC AATGCTAAA ATGTCA	420
CATTCATTT TTGATATTT ATTAGTTACT GCCAATAAGG nAAAACATAT	480
ACAAGCTATT CTACTAAGTA TAATGGTTTC CAGTTGTATC CATT	530

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

AAGAAAAAC CGTGTCATG GATTGGAAGA AATTAATATC ATCAAATGT CCATA	60
GAAAGCAATT TGCAGATTCA GTGTGATCCC AAACAAAATA CTGACATTCT TCTCAGATT	120
AGAAAAATGA CAATAAAATT CATATGGGT AACAAGGGAC ACAGAAATGC TAAAGCAATC	180
TTAAACACAA AGCTGGAGGC ATCACAACAC CATACTTCAA GACATACTAC ATACAGTTAT	240
AATGAAAACC TGAAATTGGC ACAAAAATAG AGACCTGTAG ACCAACTGAA CAGAATAGAA	300
ACTCCTGAAA TCAATACACA CATCTATGCC AACTAATTT TACAAAGGAT CTAAAACCAA	360
TCCCTAGATA ATTGACAGTC TCTTCAACAA ATGGTGCTGG GAAAATCAGA TCTCCTGTGC	420
AGAATTATGA AAGAAGACCA CTAGCTTACA ACTTATACAA AAATCTAAAA TGGATCATGA	480
CCTAAACCTA TGACTGGTAC CATCAAATTA CTAGAGGGAG ACATGAACAT GGGGAAA	537

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

925

TGCACAGATC AAGAAACCAA ACTTTAAATT ACAGTAATTG ATCCCATATC ACACAGTAGC	60
AGAATTAAAA GTGGAGTGGA TTCCCAGCAG ATTGTAAATT CTTTTGGAA TGCCACCTTT	120
TTTTATTTTG CTTTTTAAAG TGAACTGGTC AGGGATGGTG TTTAGCAAAG CAACTGTAAC	180
ACTGCTAAGA TGCCTACTAC CTCTATCAGA GTGCCAACAT TCTAGAGTCT TAGCACTGCT	240
CCCAATTCAAG CTTCCTACTA ATCAACACTT TCAGAGGCTA CAGGCGACAG CATAAGTATT	300
CGnGTCCCTA CCACCCACTT GGGAGACCTG GAGTCAGTAG TGTCTCCTGT CTTCAGCCTG	360
GCCCAGTGCT CACTGTTGCC GGTATTTGGA AGTAAATTAG CAGAAGGCAG ACCT	414

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GAATCCCACA AATGAATTG TGGATGAAAC AAAAACATAA nCTCTGGCT TGCTGAATGT	60
ACCTCTATTC nCATCTCATT TGTGTTACC TACTTAGATT TCATGANTTT AAACCTACATT	120
TCTAATAAGG GCTCATAAAAT ATTCAACAT GTATTTTTTT TCCTCCAATA CATACTTTGA	180
CAATTGATTA ThTGTTACCT AGCTATGACA AGTTTTGGC TCTTTATGGC CAGGCTCATT	240
TGGATGATAT CCTTCAGCTT GCTTAAGAGA ATTnTAACCTT GA	282

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GTCTTCCCT CTCCATCACT TTGTCACATA AATTTTTTTT AACTTTGGTA TAACAGGGAC	60
AGATGTGAAC TTTTCAACC AGTTAACAG CATTATGAA AAACCTACAG TTAATGGCAT	120
ACTTACTGAT AAAAGACTAT ATACTTCCA CCTGATATTT AGCCATGATG TAGCTATCTG	180
CTGTCAGCTT TTCTGCTGTT AATGTACTGG AGGTTTAAC CCATGAAATA AGGCAATAAA	240
AAGACAAACA AACGACTTGT AACAGCAAGG AACAGTAAA ATTCTCTTAA TTCACAGAGG	300

926

ATATGACAGT CTATAAAATT TCAAGAATT TAAACAAACTT CTTGAATTCT AGTAACAAAA	360
AGTTACTAGA GTTGAGTTA ACACAGTTGC AGGTATTTA AAAGCATAAT CTACTGTGTT	420
TCAATAAAATT AGTGGCAAAT TGGTAAGAAA TATGAAATTAA AAAACAATAT AACTTAAAT	480
ATCATCAGCA AATCCAAGAT ACTTAGGGnT AAATCTAAAA TAGTATACAC TGnAACTATA	540
TAAAATGCTA CTGAGATATT AAAGGAGAAT TAAATAAATA AGG	583

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

TGGnCAATAC AGCTATTG GAGGGATTC AGTGGATGAA AAAGATCTCT CTCACTCTAA	60
CTTTCAAATA AATAAAATATT TTTAAAAATC AAATAGAATT TCTTCATTCT TTTCAATTGT	120
TTAATTCCCTA AAATTGCCCTG CTTTCATGAT ATGATTGGTA ATGTAATTGA AGAAAATCA	180
TAGGACTGTA CCTGCCACACA ACAATGTGCC TAGCCACCTA CCCATCCTGG CAAACTTGCC	240
ATGAAATCTC TGGCCCAGGG GAGTAAAGTG CTTATATTAA TAGCAATCAG ATTTCCTTTG	300
GAGATATTAC TCTTCAAATT CACAAAAATT ATTTGATGGG GAGGCATGGG ATGGAAGGAA	360
ATGATGTGGG AAGATAATCT CAATGAAGCT GATGTTCAGC TATACCAAAG TGTGATGGGG	420
ATCAAGTAGT GAATATGCCA GGGGTAGCA CCCACCAGTG nCTCCATTAA GCCATTGGGG	480
nACCTTTGG AGTAAGGAAG GAAGCCATGG TGGTGGGGAG CCAGGGG	527

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

TTCACTGCTA GCATGATGCA GACTTACTGG AGGTATTAAT TTCATAACTG TTTGAAGACA	60
GAGTGCATTG ATTTCTATTG GTCAAGAATT TTTTCAGAAA GAATATTGAA TTCTATCAAC	120
TGCATATTAA TGGACTTATG GAATGATTAT ATGGATTTC CTCCTTGCAG TTATATTATT	180

927

GGATTTGTTA ATGTAAAATC ATCTTACAC TTTTAGAATA AAGTCTACTT GGCCAAGGAA	240
CACCCCTTTA AAGTGCTGCT AAGTATGTAT GCTAATATTT TATTTAAGTT TTAGAAAATG	300
CCAACGCCCA AAGTTAGCAC AGTGGCAGTG CCATGGCTCC GGACAGTTGG ATTATGTAGA	360
ATGGATCTTT TGCCAGTAGA TGGGATCATA GGAACAGGGC TCAGCCCCTC AGGCAGGGAA	420
CTGGTTAAAG CCACCCAGGG TGGATTCTG TTTTCATGAA GATCTAGCAA ACTTCTCTCT	480
GTTTCTGGCA CTAAGTGANA CTAGGAAC TG GGGACATT TATATGAAAC AAATGTAAGA	540
AGACCAAAGG AGACAGAGAA GAGAGCAGCA GAGCCCTnGG AGCC	584

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

TAGAATGGAA GTAAAGATAA CCTGCTAGGA GGCTATTGCA GTGGTACAAG TAGATGACTA	60
TAGTGGAAAC AAGCAAGTTG GCCTCCAAGT TCTTCTGATC ATGTACTCCA TTTCTAAGAC	120
AAATTTGCTG TTTTACCTCC AAATTAAGTA CACTTATGTA TTCCTATTTA ACCAATACAC	180
ATGCTATATA TAAAATTAAA ATGTTGAGAT TTTAAAGGGAA CAAAATAAAA ATGAAGTAAG	240
CTTTTATAGT CATTTTTAAA TTCCCTTTAT TACTGAAAAC AAAAGCATTC TTACACAAGA	300
AAATATAGTG CTTCAAAGGT CTGACACTAG ATGGACTTAC TCTGACATTT GGGTCCTTCT	360
GATGCCACAG TCACACAAAA GATACAATCA ACTACGTACC CAACTAAGCA CTAGCATATA	420
ATTTCTTTCT TTTATTGCAT TTCCACAAACC AAATATTGGA GCACTCTGG ACATAAAGGA	480
ATATTTCTT CCnTTTGGGA TAAAnCCTTTA CCAGGGATT CCACCCCA	528

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTTGGGAAAG ACTGGGGACT GGATAGGGGA TACTGTAAGA TCGCTGTGAG CTGCTTCCCT	60
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928

AGGGGCCACC AAGCATCACG GTCTAGAGAG ACAGAGAAGG CCAGGCTTGG CCCGAACATT	120
TACAGGCCCA AAGATTGTTT TCTATTCCCA CCCCAGTCCT GTCCTACATC ACAGATTGGA	180
CACCCAGCTC CTATGTCCAA ACCTCATCTA TTCCTCCAAC AGCTGCCCTT AGCCACAGCT	240
CGGGTCTGGG CATTGGGTCT CTCTGGGAGG ATGGACTGGA GCAGGGGCCG GCGTGGGCC	300
TGGAAGCGGT TTGGGGACTC TTGGACAGGG AATTCCAAGG TCGTGGGGAC CCACAGCTTC	360
TGTCTGGAAG ATGAGCTGTA GGCTGAGTGG AAAGTCCCTT GTCCCTGAGG GTTTCTTTGT	420
CCCTTGGGGA GTGGCATGGT GAGAAGGGGG CCAGAGCAGG AACCCAGTTA CCTTGAGCCT	480
CAGGGCAATC CCAGAAATGG GCTCCTTGAG CTGCACCTGA TGCTCTGACA TCAAAAGAAA	540
TACAAATAAG AGTGAACCTCC AGGAGGGCAG GCCTCTGACA T	581

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

TGGTTTAGTC TTTCAACAA AAACAAAGTC AAAGGTTGAA GAGCCTGCC ATCACTAGCG	60
GTCAAGTTTC TCCGGTCGGA AAGGCCTGGA CAGGGATAGA TGGATAGGAC CTTCAGCTTC	120
ACCTGGCTG GAGATGGCTG GGCATGGCG AGCAGAACCA AACTGCCGT TATTAGGCAG	180
CTGCTCTGTG CCTGGCCCTG GACGTGGCAG TGGAGATGAA CTGCAAAGAT GGGTAGCAGA	240
CACCAAGTTG TCAAAGAGTG GTACCAGGAC AACTCCCCAG GAAGTCAGGG AGTGAGTGGG	300
CGAGGGCTT CCTGGAGGAG GTGGGGAAC AGGGGATGGA GCCAGCCCCG ACGCAGAGAG	360
AAGGCCATCT GTGGAATGCA GAACCAAGTC CAGCACACCC TCCTGACTCC AAGGGAAGAA	420
GCTGGCAGGA GACAGGGTGA GAAGCAGGTT GGCTGGACA ATGCAAAGTC TTCAAAGCAG	480
GCTTCAGACT TGAGGTCTATA TTTTGG	506

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CGAAAAAGCT GATCTGAAAA GGCTACATAC TATATGATTT CAACACTGTA ACATTTGGAA	60
AAAGGCCAAT CTGTGGATAG AAGACAGGTT GTCAAGAGTT TGGGGAGAGA GGAAAAGAACAA	120
AGCAGAACAC AGAGGATTTC TAGGGCAGTG AAACTATTCT GATGAGAGTA TAATGGCAGA	180
CTTATGTCCT TACACATCTG CCAAAACCCC ACAGACTGCA CAATATCAAG AATGAATTCA	240
AATGTAGACC ATGGAAGATC ACGATCTATC AACGTAGGTT CCTCCACTGT AACACATCAC	300
TCTGTTAACCA GGCTGTTGGC AGTAGGGGA AGCATTGGG TGTGAAGGCT ATGAGAATTTC	360
TGCACCTTCT ACTCAATTTC ACTTGAAAC TCAAACGTGTT CTAAAAAATA TGGTCTATTA	420
AAAACAGTTT TTTAAGGGAC CAGCATGGTG ACATAGCAGG TAAAACCACA CATGTGATGC	480
CAGCAGAGGA TGGCCCAAGC ATTTGGGCCCT CTACTACCAA TGCAGGAGAT nCAAAACGAAG	540
CTCCTGGCTC CTAGCTTCGG AATGGCTCAG CGTTGGCCAC TGCGGTACATC TAGGGAAGTG	600
ACCAAGTAAA TGGGAGATCT CCCTGTGTnT CTCT	634

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

ATTTGTGCAC ACAAGATGTC CGCTGCTCCT AAGGGTGCAA ATAATAGCTT TGCCAATATG	60
AAAGCAAAAC ATAATTACTC AACAAATAAC ACACGTACA CTGGTAACAG CTGCTATCAA	120
CAGCATGTTG GAAGCCAAA CAAAGGAAGT ATTACAGGAT TTTTTTTAAA CCCCTGCCTA	180
TCATTCTCAC GGAGGTAAG TTAGTTTTG TTTCTGTCAC AGCAAGTGTG ACTAAGCAAA	240
AAGTATTTTA CTCAGTTAAT ATTCACTCT TGCTTTTAGG TCAGAAAAGA AGCTTGGCCT	300
CATTTGTCT AGCCAGAAAG TGGGAGGATG AATTTAAAG AATTACTTAG AAGATCTTTA	360
AGAAAAATCT GTTATATTAAC GCATGTAGGG ATTTnATACT TTTCTACCTG GAATATTGCA	420
GAACTACCTT TGATAACTGC TTTACTCTGG CTGT	454

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

TGAGTGATGG CAGGAGCGGC CCTCTCTCCC TCCCCATCCCC CAGATGTCAT CTGTCTACAC	60
TGCGGACACC GAGnCAGGCT GCGCTGGCCA CGTGCAGG ACAGAGCACT CAACAGCTGC	120
CGTGGGCTGA GGGAGGCTCT GCTTCTCTCC ATACGGGGTC TTTCCTCATT CCTTCACCCA	180
ATGGGGCTAT GCCAATGAGA GTGATGGTGC CCCCAGCGGA CCTGGGACAA CGAGGGGTTG	240
GTAGACACAA CGGGGCTCCA TACACCAGAC CCCCACCTCT ACCCTGCCGT GTGTCATCT	300
CAAAATTCAA AATTCTCCCC AAGAAGAGAA AGAGTAGGAA AAAGCAGCAA AACAAAGTACT	360
TCCACTTGTC AGCATCCCTG AGTAGACAGT GCTGCCGTCA TCAACCAACA CAGCCAAGGT	420
CGGTCCGGTC AGAGAAGGGC TCCCCGCAGG	450

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

CTGnAGCTGT GGCGCCACTT AAGCCCACT TTTAATCAAT AAGATTATGT CACTTGCCCA	60
AAAAAACAAAT ACAAAACAGAA GTGTTACTCT AGGATAATGT CACAATACTC TCTAATAAAC	120
CTTCCATTCA AGGTTCTTGT CACAGGATGA AGTCACACAA CTGAGTGTGT TCAAAATATA	180
AGCTACTTGA CTTTATGCCT ATTTGCTAAT GTGTGTTGT GTGTTAAAGT CTAATCCTAG	240
AATTGCTCTC ACTTGACAAC AGGTTGGGT AGAGGGAAA AGGAAAGAAC TTTAATCCTC	300
AATTGTTCA AATTTTACTT ACATCTAATG AAAGAAAGTA ATGTATGTGA CTATCAAAAC	360
TGGTTTAACT GTTTACAGTA TGCTTAGGCC ACAACATCAT TTATTCCCTT GTTATATCnC	420
TTCACATTAA AAAGCTCCAT TTTTCCAAT TCGTGTAGG CAAACTGCTC CACTATTATG	480
ATAACAAACAG TnATCATAGT TAGGATAACA AGAGTTATAA TTTTGTATG ATAnGGATAA	540
CAACAGTTAT AATTT	555

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs

931

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

AAATACTGGG ATTCACTGAGT TTGATTAATG AAGAAAGATT ATTAATTTG TGGTTTCCAA	60
AAATATGTAA GTAGAAACAA GGTCAATTAT TGTACTCAA TACAAGAAC CCAATGATTG	120
AATGACACAG ATCAGAAATA AGCCTAGGAG ACATACTAAT AACTGTCTCT GCATCTGAAT	180
AAATGAACAG TTAGTAATTA GAATTCAATTA ACCACATAGG CTAATGGATG GAATAACACA	240
ATTTTACTGC TGTTTTAAAG TTTTTGGTCC TCATTTATTTC AAATGGCTCT ACTAAGGACA	300
ACACTGATGG AGTACTTTGA CCTTTTGAC ATCACTTCTT TCCAAGGTGA AATTCACATT	360
GTTCTCTTTC TCATTAAGGT TCTGCTTGAA AATGATTCAAT GCTTGGCCGG ACGCTGACAG	420
GTCACTAGGG CTAATCCTCC GCCTGCGGCT CCGGCACCCC AGGTTC	466

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

AATCTTATTG GTATACAACC ACCATAATTG TGTTATTGAA ATTTGAAAGA AAAGGAAAAT	60
AGCAGGTCAG TCTACTTATA TGAACATAGA TGAAAAAATA TAAATAGAAT ATTCAATTAAAT	120
ATTCATTTGC AGACAATATC TAGTGAAATA TGAAAAGAAT CATGACCAAG TGGGTTTATC	180
TGAGAAATTG AAGTTGATCT AGTATGTGAA AATTAACATT CACTGTATTA ACAAAATAAA	240
AAACCAAATG ATCATTTCAG TAGCTGCGTA AATCTTTAT TTAAATTGTA TTCAACACCC	300
ATTAATGATA TAAAAAGCTT TAACAAACTT GTGATAGAAA GATACTCTT ATATGATAAG	360
GGCTTTTTT TAAATAATGG AGTGTAAATA TCATCCTGGA TGGTAAAATA CTGAATATTT	420
TCCCTGAGAT TAGGAACGTA TAGGATACTT CACCACCACC AGTAC	465

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

CATTTAACTC	GTAACAAACT	ATTAGCTACA	GTAGCACATT	ATTAAACAGA	TAATGTTTAA	60
CAATTTTATT	CACAATTGG	ATTAAATGAG	AAAAACATCA	CATTTAGCA	CCCTAAATAA	120
CAGTTTG	GATTATTGA	ATTGAAACTA	ATTCTAGCTT	TAGAAAGACA	TTACTAATT	180
TCTTAGAAA	ATTGAGGCTA	AACTACTTA	GTTCTCTCT	TTTTTTAAA	GGCAGACAAT	240
TCTATAAGAT	GATATGGTTA	ATTGTATT	TATTGTAGAT	AAAATTATG	TATCATCAAC	300
TTGGCAACCG	GTCCGGAAAT	GTCCATGGCA	AGTGATTAC	AGTTGCAGGA	GAGAAAGCGT	360
TCTCTGCCAG	GCGGTTGAGC	GTGGAGG	GGGGAAACCT	GGGGTTGGGG	CAGATAAATA	420
TTCAGCAAGT	TTACTTTGT	GTTCAGnATTC	ACTGCCTGCC	AAAGCCTCAA		480
ATTAATCCAA	TTAATAATAT	CTAAGTAnGT	GAACTTACAC	AATCCATAAT	CTA	533

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CAGATAATT	AATTAGGCAC	TTCAAAACGTG	CAGTAAGATG	GAAACTTCC	ATTTGAATAC	60
TTTATGAGTC	TAAGAGGGCT	TTGGAGAAA	GAUTGGTAA	GAGTTAAAC	TAACTAATT	120
TCAGAAAAAA	TGATACCAAC	TTCATGCTTA	AACAGACTTG	TTAAAAGAC	TATCTAGATA	180
TTCATTATTG	TACACCAAAT	ATGAAAACAA	AATATATCTT	GTTCATTAA	ACTCCCTTAC	240
TGGATTATAA	TTTAAGTATT	ATAATTACT	GATGTACTTC	AGTTGTTAAG	TTTCTATGGA	300
GACATTACA	TGGTATTAT	AGAACCACAC	ATTAGTATGA	CTTCATAAAT	GTAGCAGATT	360
TAAAGCTGCA	TCCCACATCTAG	ACAAGGATGG	TATGATCTCA	CTCACATGTG	GAATCTTACA	420
AAGGTGATCT	CATAGAAGCT	GAGAGTAAGA	TGGGGGGTTA	CCCGACACTG	AGGAGA	476

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GTTTCTGAAA	TGAGGCAC TG GGGGATGAAA	TAGAAACACC	ACTGTATCCT	TTAAGCCTGC	60	
TCTGCAGGTC	TCCCTCCTCA	ACCACCACTG	TGGTTTCCTT	CCTCAGGTGG	TCGGGATGGC	120
AAGGCAGTTGG	TTGACTTAAC	GACAGGCGGC	TGTTCTTCAC	TGTGTTCCAT	AACTATAGCT	180
TGGAACGTCT	TGTCTTCTTT	CCAGACTACA	AATCTGTATG	TTTGAGCTA	TATAGAATT	240
CAAAGGGCGT	TGATAAATAA	TGAAAGAAAA	CAGAGATTTG	GGGTTATTTA	ATGTTTTGTA	300
TCTACCACAG	ACTTCTCTCA	AAAGAGAGCT	AGATTTGTT	AAAAATGAAA	CTTCTACAGG	360
AAAGAAAAGC	TGTCTATATT	TCATGAGAAG	TTGTCAGAAC	ACAAAAAGGA	ATAATCTTT	420
TTTTTTAATC	AATCTGATCT	GTCACAGAGA	AACAGAAAGA	GTATCTCATC	TAAnGGGAnT	480
CCCATGAATG	CCAAAGTCCC	GGGGAAAGCCA	GGAGACC			517

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTTAGATGT	ATTGCTGGGA	TATAGGTATG	CTTTAACATA	TGCAAATAAA	TGTACGGGAC	60
ACGCTACAAA	GTAAACAGAA	TGTAAGGTAA	TGTGATATAA	TCATCTTAGT	TATTTAGTAA	120
AATCATATAA	TAGAACTCAG	CATTCTTC	TGATAAAAAC	TCCCAGCAAG	TTAGGCATAG	180
AGGAAATGTA	TCTCAGTATA	ATAAAAACAA	TATTTACAA	ACCCATGAAT	TATCATAATC	240
CATGGTCAA	AAAGTGGAAAC	TTTCTTCCTA	AGATCAGGAG	CAAGACAAGG	ATGCCAACTA	300
TTACCATTTC	TATTAACAT	GGTGTAGAA	ATCTAACCA	GAGCAATTAG	GCAATAGAAA	360
GGAGTAAAAT	GAATGAGAAT	CTAAAAAAAGT	AAAATTATCT	CTCAGGTGGC	TGATCTTATA	420
TACAGAAAAT	CCTAAATACT	ACACTAAAAA	CCTCATAAAA	TTATAAAATGA	AATCATAAAC	480
AAATCCAGCG	TGTTTCTATT	CTCTAACAAAC	ACACTGAGAA	AAAAGATGAA	CA	532

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs

934

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

TAATTCATn	TGGTTTGAT	TTGnACTTGA	TATTTTCAA	CTAAATATT	ATTTTGAAA	60
TAAAATATT	TAAGTTACAT	TATAGTCACA	TTCTTATGT	GCCACTAAAT	AGAGTTCAAC	120
AAATAAAAG	TGAAAATACT	GTAGTTAGC	AGAAATATAG	GCAAAGCTCT	ACAAAAACAA	180
TCAAATGAAA	AAGATGTTAC	ACAGTAAATT	TTTAAATAGT	nACAGATCCT	TAGAACTGTA	240
GTGGTATATA	ATTCTTAACC	ATTGATGTT	GAAnACCTTT	TTATAATCTG	ACCATTnAA	300
AGTCCTTGA	GAAATGTCTA	CTGAAATCCT	TTCCCTCATTT	TTTGTGTTGGA	nTTTTGGTTT	360
TTGGnTCTCC	AGTTTTTATT	ACTTCCTGT	ATATTTATA	CAGTTTAAC	AGTTTAA	417

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

AAAAATCAGT	CTCATTATTT	ATTGTCAGAC	TTGATGCATT	CAATATGGCT	GATGTGTGAA	60
GTTGAGAGCA	ACACCAGAGC	AAACCCATTGC	TCAATTCCCT	GTCGTGCTGT	CACCTCTTTT	120
CCTATGACTG	TCTAACAGA	TGGTCCCAGC	TCCTAGCAAA	TCTTACCCCTA	CTTGAGGAAG	180
CAACACGTCT	ATTTTCAGT	GACAGTTAAA	TTCATGGCCA	AGTGCACTGG	ATTCCATCTC	240
CTTCTTACTA	TCATACCTGT	GTCCTCCACT	TCTCTCTCAG	CCCCTATCTC	ATGCTCTCCC	300
TGTAATTTTC	TTAGGCTAAT	GTAATTCCCTT	CCTCAATAAA	GACCCTTTG	GTCTTCTGT	360
ATTGGTCTGA	CACCACCTCA	ACCTGGATCA	GTTCTTCATG	ATTTCCAAAG	TGACACAGTA	420
AAGATACATC	AGGATTG					437

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CTAATGTATA AGCACTCATC AAGCATCCAC TCCCATCATG CTTATCAATA TCCCAGTGGT	60
CAAAGCCAGT TGCACTGGCCA AACCCAGGGT CAGAGTTGGA GGGGCTGACA TAAAGGCTTG	120
AATGCTGAGA ATCCCCAGTTT ATTGACCACC ACCAACATAA CAGGCTTTAT GAAGAAGTAT	180
TAGGGCAAGG TTCTGAGAAA CCAGAGAGCA TTTTTCTTCT CCTGTTATCA GTTATTTTT	240
CTTCAGTACC TTATCTGTAG AACACTTGTAA AGCCATAGAA GATAAAGTTA CTCATCCAAC	300
ATCAGCATAA ATTCTTAACT CTTTTAGCTG CTAGAAATAT TTCACAGAGA TAAACCTGTAA	360
TCTGGCTTGT AGGAGCTGTG GTCCTATCAG AGAGATGCGT TTGCAAGCAT GCATTACAAG	420
ACAATGTGCA CGACAAACAAA CATGTATACC TCAAGTAAAA AG	462

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GAATnGAGCT CGGATACAGG AATATGTATT GGAAATAAAA GACATGAGCC TCCAGATTAA	60
AAGGACCTA CCAAATGCTT TTGAACGTAA TTTGTAAAC ACCCGCCCAA GGCACCTTCAC	120
TATGAAATTT CAGAGACAGC CTACAAGCTT CCAAAGATAA GATAATAAGT ATATTCCCTA	180
GGTGAAATCT TAGATTAGTA TTATGAGTAT ATGACCAGTG GAGCAATAGT TCAGTGATTG	240
TTTACCCAGC TAAACGATCA ATCAAATGAA AGAATATTTT AAATCCTTTT CATCCTTGCA	300
GAATATCAGA AATTTGCCTC TATGCACCCCT TTCTTAGAAG ACCACAGGAG GAGGTATTAA	360
CACAAATGGC AGGGCAGAAT AAGAAAGAGG AAACTGGAGA TCCCGTAAGT AGAGGTTATT	420
CTTCCAACGA AGAGGCATGC TTTTGAGATA GGAGGTGAAT GGTGTAGAAA TGCATTTGA	480
CTCAGTAGTT GAAAGTTGAG AGAATTACA CCTCTGTTTT CTCAGTGGGT GAATGCAGGG	540
nTGCTTACTG TAGTTAGAAG CTTTGAGAAT AGACAGACTT GGGGGACAAG AAAAGGGTCT	600
CATAACCTGG GATAAAACTA TTGGnCAGTT TGGnATTGGG GGG	643

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TATACTTCTT CATTGACTCA AGCCACTGAA ATTTTAGAGG TTGTTATTAC AGCACACACA	60
CAGTTTCCC TGACAGACAC AGATTCAGGT CTAGGAAGGC CATAAATGCC ATATTAAGGA	120
ATTCGAATTG TACTCTGAAG GAGGTGCAGA GATAACATT TTGAAAGGAG TGACACGATG	180
TACATTTGAG TACAATAACT CTGGATACAA CATACATAGT ATATTGAAAA CAAGGTGACT	240
TTCAACCTTT GGTGTACATA AAAATCCCCC ATGAAGAACG GTAGTCACAT TCCAATTCCCT	300
ACATATTACA CACTCTATAA AGAAGAAAAT ATTTATCCTC TGGGGAAAAA AGTTACCCAG	360
GAATTCTTCA AGATGCAATG CTCTGGGCCA GGATATCTTC AGATATCCTG AATCAGCATE	420
TCTAGAGGTG GGGTTTATGC ACAGTAACGT AnAGGACAAG CTGAGTTCAG AGGTAACCAA	480
ATTCACATGC TTGTGGTTCA AATAATCATT CnCCCTCATG GAT	523

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

AGAAAAAAAAA ATACTGAAA TATAAAGGAA GAAGGAAGCA AAATGTAGAA ACTGATGAAA	60
TAAGAAATGT ACAGCGGTAC AGCTTACCCA GGTATAATCA ACACAGTCAC CACCAAACCTT	120
GGAAAAGAAC TGAAAGTGAG AGAGCAAAGC ACGAACAAAG ACAGCCAATG TCAGTAATGT	180
AAAAGTTGCT ATCATTCCAT TATCCCACAG ATAAGGAGAG GACATTATGA AAAAATTAT	240
GCCATTGAA AATATAGATG AAATAAAAAA GTCCCTAAAA TAATACAAAT CACCAAAACT	300
ACAAAGGAGA AAAGACATAG GGCTGTGACT CTTAAAGATA TTTAAAGTCT TACATACAAA	360
AATATTCCAG GCCAAGATTA CCTCCTCTGA GTTCTAAGAA ATGTTGAAAG AACAAATAAC	420
ACCCACCTTA CACAGACTCT TCTCAAGAGT AGACCTCCTA CTGAGGTCAG TGTAACCCnG	480
GAACCCGGCC nGnGCAnGGA CGTTGTAAAA CAGGAAAATT ACAGGGCTTG ATTTCTATAAT	540
CAGAATGAGA AAATCTTAAA ATAGCAAGAT ACAGGAAATA ATATCATAAT CA	592

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TTGTGTTTC	CACTTGCTTC	CGAGTTGCAC	TGTTCAAGATA	TTTAAATGT	CCATGTGACG	60
CAAGGCTCCT	AGAAAAGTTC	ATGGAAATGG	ATTTTAAAC	ATTGACTTGG	GCAAAAACGT	120
TTGGAATCC	ACCTATGCAG	ATAAGGGGTC	TTCAGAAAGT	TCCTGGAAA	ATAGGTAGGA	180
AGAAAAAGTT	ATGCATGGCG	TTCCAAAACA	TTCCTTTGC	ACCAGAATGA	GCTCAGTTT	240
TGACTCCTAT	TTCCATGCAT	TTCTTAGTCT	CTCTGTATT	TCTCCCATT	TCCTTTGCCT	300
TGGAAAACCC	TAGTGTAGAG	TGCATTTCTT	GTCTGGAGAC	ACAGACACAA	TCTTTCTCTT	360
TGGAAAACCG	TGTGTTGAAA	GAGTGAGTTG	ATGGGGCCGG	CGCTGTGGTG	CAGCGGCTTA	420
AAGCCCCGGC	CTGnAAGGCA	GGCATCCCCT	ACGGGGCGCCG	CTTCGAGTCC	GGGCGCCGCT	480
TCGAGTCCCG	GGCTGGCTCC	TTTTCTGATC	CAGCCCTCTG	GCTATGGCCT	GGGAAAGCAG	540
TAGAACACAG	CCCAAGTCCT	TGGGGCCCT	GGCACCTGCA	TG		582

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GTAAC TGCCA	ATACCCAGTC	CTCAGCAAGA	TTCCAGTTCA	GTTGTTCAAGT	TATCAGTGTT	60
GATTAAATG	CTCCGCAAGT	GATTCTAACT	GCAACCAGCG	ATGAGAAAGTC	CTTTAGGTTT	120
CCCTGGAGCT	AATAGCTGTC	CTTATTTCTG	AAATCAGTCT	TAGGATTCA	GTGACATGCA	180
AATTAAAGCA	TCTTAAATAC	GGACCGTTT	CTTGAGTGC	AATGCAAGGT	TCAGTGTAA	240
AATTTTCTTT	AATTAGAACAC	ACTAGGAAAC	TTAAAATCTC	ACTTCCTGGC	AAAAGAATTA	300
GGCTTGCTCA	TTTATTTGAG	AAAAAGATTA	TGTGCCTGCC	CAACCATCAA	TCCTAATTCT	360
GAAGACCTTG	CACTGnAGGG	ATGTCAAAAG	AGGAGCTGGT	GACTAACAGG	AGGGACTGAG	420

938

GGTAGGGACT TTGnAATATG GTGAGGAAAA AAAAAATCAA TGCCTCACTT ATCCTTGGC	480
AACAAATAGA TATTAATCGT TTTAACACTG ACCAGTTGGG ATATTATTTT GTTGCCCTACA	540
GCTGAGTTA AGATCCATAA TTTCACATAG TTGTTCCAGG An	582

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

CAGnAGCGGG CGCnGGCGCC CCCAGCCCTC CTTCCACCCT TGGAGCTCCC AGGCTGCCTG	60
GCAAACCCCTC TCCTCCCTCC CTGCGCCCCA CCCCACCTCTC ACTTCCTCTT TTCTGGTCCT	120
CAAAGGTACC CAGCTGCTCC AACCTCGGGG CCTCTGTGTC CGCTGTTCCC TCTGCCTGTA	180
ACACCCCTCC CAGGCACGCT GCCAGGCTGA GTCCTTCTCC AGCCGGGGCC TCCTCCCTGG	240
AGCTGnnCCG CCCTGGCCCT CCCTGGTTAA TCAGCGAnnc CCACCCCTTC ACCCCCAGCCC	300
CAAGTCGCAC CACCCCTGCTG GACTTCCTCT CTCCCAAACC GTCTTGTGTTG TGAACCTGTT	360
GTGGTCACAG CTGTGGnnCC GTGCTC	386

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

AATGAAATGG AGTAGAGAAG AGACTTTCA GCCCAGCAGG GTCTCCCTCC TGTGCGGACG	60
TTGTTCTCGG GGATCTGCGA CGGGAGCTGT GGGCACTCGG AGCCGAGACG CAAAATGAGG	120
CTCACAGACC AGAAAAGGGT GCAAGCCACC GTCGCTGGCA GCCGCGGCCG TGGCTCGCCT	180
CGCTGGCCCT TCCTAAGGCC CCGCCTCTGC GTCCCCCACG GATGGAAAGG GTGCAGACCA	240
CCGAGCTCCG AGATTGCGAG AAAGAAGCGG CTTGGGGAGG CCCCGCGGGG AGGCTGGGGG	300
ACTTCCTGTT CCGGTCTACG CCAGGCGCAG CCAACACTCG CAGGAGCTCA GCAGCCCCCA	360
CCTGGTGACA GCCTGGGTGG GGCAGGGAGC CCCACCCACCA GCGCTGCTT GCTGTCCCC	420

939

ATCCCTCCCCA CACACAGGGG ACAGCTCCTA GCTGGCTGCT GAGGGTTGGG GTGGGGTGGG	480
CATGGTGGGG TGGGGAGAAAG GCAGCCCCGG GCTCTGGTGA CCTGCCAnG ACCTGCCCGG	540
AAGCCCTCTG TACACTGCCA CTGGTTAAC TCATCACAAAG TTCCGCCAG AGCCCTGCAC	600
TAGGCACGTG GTGTTGAGTT CATGGACCT GCACCACAAG CTGCACCGCG ATGGGCACAT	660
GCG	663

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

TGCAGGATGT CCAGCGTAAn AAAAGGGTTG GGGGGATAAT TGTACCTCCA TGACAGGCTT	60
CACAAACTCC AGGAAGACGG GAAGGCCTAA TTCTTAGAAA ACGAAACTTA GTATATACTT	120
CCTGAAATTa ATGGTCTCCT ACTTCCTTGT GTGACCACCTT CCTTCTGAGA CGCATAGTCC	180
TGGACTGCTG AGATGCACCA ATAAAATGCT CAAATTAGG TAATTGACAT ATAAAGAATA	240
AGGAACATAGC ATATGTGCAT AATGACGAAT ATACTTGTTT ACTCAAGTGT ATAACAACTC	300
GGAGAAGGGG AGAGGCGGGG CTTCTCACCC CCGGCACTrn CACTATGTTc TATGTGTCGG	360
TGGGAGCCCC AGCTAGCTGG TAATAAAACA ATAAATCTCT TGGCCCTTGG CATCTGTGAC	420
TGTCTTTGT GGGTTAATGG GAAAGATCTC AGATCCCATA ATTCAACACT ACATAGGAAA	480
CCTGGATTGA GTTCTCAATT CCTGGGCCTT GGTTACTAAC ATTTGAGGGA GTGAGCCAGA	540
GAG	543

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CTGGAATATT TCCCGTAAGT TAGGTATGGC ATTTTGTTTG GGAACAAATC AGAATTGTT	60
TCTTCATAT TAAAGTTATCA TTTCACCTAA ACTACAAGTT GACTTCCTGA ATTGAGGTCT	120

940

AAAGCTCTTC AACTCTGTAT ATTTAAAGAA GTTTATTAGA TAAAGAAGAG ATTTATTTGT	180
AATTTTAAGT GCTTTAGAAG TAGGTTCTAT CTTGTTCTGT TTATCTTTGT TGTATCACAT	240
GCTATGAATA TTTTAAATGC ATATACTAGT GAATAAGTTA AAGAAAAAAA ATCAGTGAAT	300
GAACCAAGGCC TATCCGCCTG ACAAGTTTC CATCCATTCA TTTCTCTAAA GCATTTCCCA	360
GTCAACCTGA AGTTTCCCTT CTGAAGTTCC CCTACAAAAA GGCAAGGAAT GGAAGAAATG	420
AGAGGAGTGT CTCCAGGGAT GGCAAGAGCTT TGGCCAGCAT TGGCGTAnA GATGAATCTG	480
CTGCTGTTG TGGGGGAGGA TTGAGTCCTG CTCATCCTCT ATGCAACCCT AGTCCAGCTT	540
TCAGGCGTGG nTAACCCCTT TTCAGAACATGT AGCCAGCCCCA GGCC	584

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

AGGCCCCACC TCCAAATAAC CTAGGAATCT GGGGACTCAG TTTGCAAAT GTTAGCATCC	60
AATGGTTTGC TTCAGAAATG CCTGAAACAG CTGGTGTACG GCTAGGTTAA AGCCAGGATC	120
CAGGAACGCA ACCCTGGTCT CACATGTGGG CAGCAGATAC CCAACTACGT GAGCCATCAC	180
CTGCTGCCTC CAGGCTGTGC ATTAGTAGGA ATCTGGAATT AGGAGCAGAG CCACCTTTGA	240
ACCAGGCACT CTGATATGGA ACACGGACAT CCCAACCAAGT GTCCTAACGG CCGGGCCAAG	300
TGCCTACACA TGTCTCATT TTGATGCAGG TTTTTTTTTC ACTCCTGGAT ATTGGTTTTA	360
AATCTTATC CCTCAATTCA AGCAGCTCAT GGAAATATAG CATTGAAGA CGTACCAGGA	420
GAACGCACAG CTGACCAGCC AGAGCTGAAA TGTGCATGTT GAAGACTGGA ATGGCTGTGG	480
TATCAACAGA CTGCAAGCTG GAGTCCACAG TAGATCCTCT GCATTTCTCA CTCACTGGGA	540

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

941

TGCAGGTTAA GAAAGTACTT TTCAAGTTAC TTATCTGAAA ATACATCTGT CTAGAGAGCC	60
TCAAGATAAA AGAAATGTTG CCAAATTTTT AATAGAACAC AATAATATGG AAAAGCCTAC	120
AGCACTTCCT CTCCAAACTC CTACAAAATG TCAATGGTGT AGTCAGCAAG TAGTCAGAAT	180
TCTGTGAAAA CCATCGTAGG CATAAGAGAC TCTTAAGAAT AGGAAAAAAAT ACCCACAGAT	240
GCTTAATTGG TGAAAACGTG CTGTAAAGTA TTTCTGAACA AACCTTTAGG AGGCTGAAGT	300
TCCTTGTGGA AAGCCCTCAG GCACCTGTGG TGAACCTGCA GTGGAAGTTA ACCCCAGGCG	360
GAAAATATGC TTCCCTCACCA CTATGGTCAA AGCAACGAGG GTGGAGGGCA GGGACATCTG	420
GACATTAGCA AAGATTCTGC TTTGAGGGAC AACTGTCATA AGAGCTCCAG GCCTACGTCA	480
AAAGTGTCTC AGGAGAGGGG TGGGTGAACA AGCT	514

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

ATAATGAGCA TTTTCCATGA CGTTTTGTGTA GACGCCCTCA TGCACAGGAT TCCTGGGAGC	60
TGGTCCGTGG GGGCAGTGTG AACCAGTCCC ATCCTATGCC TCAGAGGTGA TTTTTTCACG	120
GAAATCTGTG GAGTGCTGCT CCCAGGACTT GTAGGCATCC ATAATGGTAT AGGAAGGCTT	180
GTCCTTGGT CCGTAATGCC TTCAGTCCCG TGGCCTTCCT CAGATTCTGA CGGCGCGCAC	240
CCATCGTGTG GGGGACTGGC TGGACTGGAG CATCTGCCAG AGGATCTCGG TGATCACTTA	300
GCATGAGTGA ATTGACATGG CTGTTGAGA GCTTTGGGC AGCCATTGTA ACGTTGTGTA	360
GATAGGGTAC CCCAACACT GGGAGTTGC TACTTCATCA CGGTGTTAA GGTTCCGTGAG	420
AAGTGCCGTA GTCGCCTGTG GTTCTCTGAT CTCCAGAATG GATAAGAAGT CAGCCCTTAA	480
AATGTCCCCA AAGCTTCAGC CATGTTAATG AAGCCGGATG ATTTACAAGT ATTATTGGnA	540
CTTTAAACC AGCCTGGCTG CTGGTATACA TATAATTCTG ATCTTACTTT ATAAATTTC	600
TCAGTATGTA CCTTATGAAG ACATTTTAA TTG	633

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

AAAAAAA	AAAAAGTAA	TGACTTCTAA	TCTCCATAAT	TAGGTCATGG	TTTGGCCTTT	60
ACACACTCCC	ACTTCTTTG	TCAACTTCTA	GCAAGAACAT	CACAAATTTT	AGAAAACGGT	120
ATTTAATT	TTCATGGACT	TAATGATTCT	CCATCCAGCC	CTAATGATCT	CAGTAATTAG	180
TACACTAAC	TAATACACTC	TTTGTAATT	AAGAAAATCA	CTGGGAATT	AAACTAGCTT	240
CCTATTTGAA	TGAACATCCA	TAATCATGCT	TCTAGACTTT	AGACATTAC	CTGATCCATC	300
TGTTTCACA	GGAAAACGAC	CACTAAACAT	AGACGCCAGC	ATAGAGTCTT	TGAAACGACA	360
CAAGGACTCA	CGCCGGGCTG	TGTACGTGCA	GCCACCCACG	TTCAGCCGGA	GAATATCTAG	420
CACCTCTGTT	TCTGCCTTGG	GGCCTGCCAT	TGCTGCCTCC	CAGCGTTCGC	nGAAACCTCA	480
AGGCAAGCAG	TCCTGGTCCC	CCTCTGTGAA	AACA			514

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

TAnAGTGCAT	GTTCCTGTG	GGCCATATT	AAATCGCTTC	ACTACATTGT	CTCACATAAT	60
CCTTTCCGA	TAGGTCACTG	GGCCTTAGGG	GCCTTAAATA	AATTGTCCAA	AGTCAAACGA	120
GATAGCAAGA	GGCAAATCTG	GGCTTGCAC	TGATGCTAAC	ACTTTCTAAA	GTCCACGTTG	180
CATGCCTGGG	TGATGCTTGA	ATGCTCCTCT	GCACATT	CTTTAACTC	TGCTATTACC	240
TTCTTGGTAT	TGTATCATGA	TTTATTGGTG	GGTGAGTCTT	GTCTACCCCA	GTAAATTGTA	300
ACCTTCTCAA	GGACAGGGAA	TAAGTTATTC	AAGCCTATAT	CCCTAGCACT	TAGCAAATTG	360
TCTGGCACAT	AACAGAGCCT	CAGTAAATGC	TTGTGGCCTG	AATAAATAAA	AGCCTTGAGA	420
GAGATGGTCA	GGGAAAAGCA	GACAGAGTAA	TCTAGATTGC	AGTTTGAACA	AAACACCTCC	480
TTTCCATGG	nCCTGATTAG	GGAGGTGTCT	GCTGGGCATG	GAAGGCAGAT	GGGTGAAGGA	540
GCAGGGACAG	CCATGCCTT	CCCTGGTTCT	CTGGAAATCC	GGCT		584

(2) INFORMATION FOR SEQ ID NO: 366:

943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

CAAGTGATCC AAGCAAATG AAGGCACATT GCATTCACCC AATTTCTGA ACCAATCTGT	60
ATTGGTTTAC TTTAATTAAC AACATAAAAGG CTTGTATACA TAGAATTAC TCTCATTTT	120
ATAAGACCAC TCTAGCTGGA AAGCAAGAAC ATGAATACAA CATAGGTCTT ACATCATTAA	180
CAACATTTA ATGCATTTA CATAATTGAA ATTGACTTAA AAAGCTGTTA CTTTATCAAA	240
TTTAGAGTCT TCTCCTTGA GAATTCCAGG GATCCTACTG GAAGCCTCAA AATTGGAAGA	300
CTCAGTTAG GGCTTAAACT ATCAGAGAGT CAAACTATT AGCCAAAAAT TAGTATGTTT	360
AACCTTGAAA GGAAACGGCTG AGAGCCGAGA GCCAAGAGCC GCCATAAAAA AATGGCCTTA	420
ATGAAACAGT CCTGGAAAT GGGGAGTAAA CTAAGTTCAC AG	462

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

CTTAACGTAACCTATTGT CTGAATTCC CATTACATTA AGAATAATAT CTCATCGATT	60
CAAGCATTAA TTATGAGTTA AATAAAATAT CTGACAAGTG TTTATATCTG TGAGAGTCAG	120
AATTCTATCC TTTTTAAAAA ATTAGCTCAG GAAAGTTCTA TGATTATTAT CATCTTATAA	180
CACAAGAAC TGAAACTTGA AAAATTAAAG TGTCTTGCCC AGGTTGTTA AACTGCATGG	240
CACTGGACTA TGCTACAAAT TAGATTCTT GGTTTTCTA CATTGTTATC TCAAGTATCA	300
GTGACATCAA GAAACACAGA AATGTGCTAG AAAAGCTTAA AAAACATTAC AGCCTATAGA	360
ACTATCATAT AATTAAATTA GTGAAGACAT CTTTACCCAA CTAATTAACA AATGAGATGG	420
CTTTCAAAA AAAAGTTAAG TTTAATTTC AGTTCAAATA AATGAATATA TGATGTATGG	480
GGGTGTGGAG GCAAAAGTTC CTGAATCCTA ATTCCAAAAG AGAGTTAAAA AAAGAGGACC	540
CTGGCAACAA TTTTGGnCCC ACAATCATT GTGGCCCATT ATGTGCTGTA AGAAATACTT	600

ACTGAAAGCTT TTTT

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAATAGAG CTCTGACTAT CACAATCACC	CTGGAATCCC AGCCTGGGA AGACTCATTC	60
TTCCACAACC CCATGGCTGC AGAGATGTGA	AGAAAACAGC AACCCACAGA TTAGAGGCC	120
AGCCTGACTG TGACATGCCA CTCGTGCTGA	CATTCCACCA GCCAGGGTAA ATCACACAGC	180
TGTACCTGCA TTCTGTAAAG TGTGGATGTA	TAATCTTCT ACAGAAAATG ATATTCTGAT	240
AGTGGTGAC AATAGAACGTC CACCACAGGG	ACAAGCCTCA GGAAAGGACT CAGGTTAAC	300
CTCAGCCACG TGGAATCTAA GGTTCTGGC	ACATTTCCTAA GTTAAGGAGG AGTCAGACAA	360
ATATGGCTGT ATCTGTAGGG TGGGACTCAC	ATAAAACAGG TGGAAATAAG TTCAAGAAC	420
CAGTGGTAAA AATCAATCAT GGTAATAAGA	GTAAGAACAC CTACCACCTA TTTAACATCC	480
ACCCCTTTGA GTCAGACATT TTACATACAT	GTTATTCTCA TCATACTTTA CCATAAAATTA	540
TTGCATTCCC TTATATAATC TATGCATCAT	TTTATCTACA TAAGTATTCT ATGAGTTAAA	600
TGTTTCTGCC ATTGTATTAC AGAAGTGAGA	CTGGGAGTCA GATTACATCA CTTAACCCAG	660
GTCAAAAGGC AAGAAGAAGG CAGGGAGTTG	AACCAGTTCT G	701

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

TGCCTTATTT CTGTAGCTGG AAGGCACTCC	ATGATGTCCA GATTTAACTG TTCTTTCTCA	60
TAGTTGGAAT ATTTTTAGTG ATTGATGACA	AATCACACTT TAATTGAAAC TCTAGAAGGC	120
AAGAGGCTCA CATTAAGTGA ACACGTACAG	CAGACATGAA GGGGAAGAGT GTCTTCGTTA	180
TGGGTGTGCA GTTTGGCAGA AATGATGCC	TGAGTGCATG TTAAATAGTC TAGCAAAGTG	240

945

AAATCCCACA GCTCAGCTGT GAAAGTCAGTG AATATAGCAA TCTGTGTGTG GCAGAAGCCT	300
TCACAGCTGC TCCTCCATGG TGCACTCTGA CTTGGGGATT TGTTTTGTT ATACAGCTCA	360
CTGGGCTCTC CATAAGGCAT GAAAGAGAAA AGTTTGACTG ATTTGCAGCA AATAACTCTT	420
TAGACTGCTT TCTATTGCAT TGGAAGCCTG CTTTAGAGTG TGTAGATGCT AAATAATGG	480
TAACCTGTTCT ATGTTTTATT TTTATCCCTG GCTTCAGCAA CTTACATTTA TAGCATAATT	540
TTTGATTTCT GCCTGCATTA GAGCAGGTAG GGAAATATAA TTAAGAGCAC ATTTGATTCT	600
AACCTGCTCC TATGG	615

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TGCCGATCAn ThCCCAGCCC CGTATCAGAG AATCGGTTGT TAAATGTTTA CCGACACACC	60
ACTGGCTTG GTTATCATTT TCTTACTTCT TTCCCTTATTA GTTGCACTAG TTTGCATACC	120
CATCAATGAT ATGATGGTC TTTTTTTGTA GTTATAATTG ATTATTTCT TTTAAAATTA	180
AAGTAGTAGT CATCCTTCCA TACAAGGAAA CGATTGGAAG GAAAAAAATC ATAATATTCA	240
AAGATAGGCT TTTGGTGAAC AAAGCAAGTA TGGACTTTGA GCTACATGAG ATCTTCAGAA	300
AGTGCTCAGA ATATATTTTT TTCTACAAAG AAACCTTTTA TTTAAGGAAG ATAAACTTCA	360
TACATTCAT AAGTACGATT TTAGGGAATA TAGTGATCTT CACACCATACT CGCCCTTCC	420
AACCACTCTC CCTGGCCTTC TCCGTCTCCC TCTCCCGTCC CCTGnCCCCT TCAACATGGA	480
AGATCCATTT CAATTAACCTT TATAAACAAA AGGACCAACT CTA	523

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

ATTAGTAGCA TGATAAGTCT GCCAAATTA ATTTAAATAA ACTAAAATAA TTAATTCTCA	60
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946

GTAAATATGA AGCATCTACT GAATAAAAAA TCGTGGTTAA CAACACATAC TTCCATGCT	120
TGTGAAACTT ACAATCTACT CAGGTGGGT AAGGCCAGAA TATATGCACA ATACTAACGG	180
ATTGGGGTA GGGAAAAAAA TCTGTCCAAG GAAGGGACAA ATCTCAGAGA TACAGAGTAG	240
GGAAAAGCCA GGAAAGAGCA TGTACCAAGT CCTAAAACAG GAAGGGACAG AAATCCTGGA	300
GACGACAGTT GGGATGGCTG GAGAATGCAC CACCCTAACG GCAACAGGAA TCATTGCGGC	360
GGGGTGGGA AGCTTTATTC TGCCAAGGGC CATTGGATA TTTATAACAT CATCCACAGG	420
CCCTACAAAA TTCTCAACTT AGAAGTCTGC CTGCTCTAGA TTTATTGCAT TTCAAGTGCC	480
GCTTGAGGCT TCCTTGGCAG GGCAGACCAA ATGACCTTGG TGTTTTATAC GGCCC GTGGG	540
CCAGAGGTTTC TCATCTCTGC ACTAAAGGGT TTGAGCAAGG AAGAAA	586

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

TGGGTTTATA ATTCTAACCA AGCACACAG TAAATCATT CTATATCTAA ACTGTAGCAC	60
TTTGAAATTC ACAGAGTAGTT TTGCCATTG GGTATGTTT TTACTGTG GTTTTTAAAA	120
AGTCACATCT GGTGCCATT TATTGCTGTG AAAGAACCGC GTCTTCATTC TAAATCTAAG	180
ATAATATTCT AATACTTTTC CTCAAAAGAG TTCTTAAAAA TTTCTAGAAT GATCTTGCA	240
TAGTTTCCCA TTCACTGACT CTGTAATGAA TAAATATTG AAGCCATAGC AATAATTTT	300
CATGCATATG ATACTGTCTT AATAATTCCG TTGTGGCTAT GCGCTTTATT GATTTCTGTG	360
CCACTTCTGT GGCCTGAAGT GAAATGTATT GCCCCACGGA AGCCATTATG GTTCCCTTTC	420
GAATTACGGC TTCACTGGCT CGCTCCTGTG CGCGGGCTTC TTCTCTGTCT GCAGTGCCTG	480
TTGGTCCCT GGGAnTTACT GGGGnCCTGG ATTCCCCCCTA TCGCCCTCGC CTTGTCCCTGT	540
GnGTGGAAGA TGAnGACAGG AAAGTTGGGA AGAAAAATGC AGCAGGCAGC CAACCCTGGA	600
GAAACCGCTC TTCAGACTTC CGGGnCnCCT GGGCGATGGG GCATCCTTCC TGCAAC	656

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

TAGGTTGTGT	nCCAGAATTG	CAATCTTCAT	CATGTACTGG	GGCTTAGAGC	TGCTCTGTT	60
CACACCTTCT	CCCCCCCAGA	AAAAAAATCCC	CACTGGACAC	AACAGACATG	CCTGAGAATT	120
TAACCACCTT	GCATATATAG	CAAATTCTT	CACTTATTAA	TACCCACGTA	ATTTAATATT	180
ACTAAACATC	AAGCAAGTAT	GTATTAGCAT	CAACTTCTTG	CTAGACAGAC	ACTATTTAG	240
AAGTTGAGAT	TCAACAGTAA	CTAGAGCAGA	TACCAATACC	TGCTCCCAGG	GGTCTTACAT	300
TCCATACAAA	GAAGATAGAC	CATCAAGGAG	GAAGACAGAC	ACTGGTAGGA	GGGAAGTCCT	360
TCACCCAAAG	CTTTGTTCT	TGGGCCAnC	TGGCTTCCAA	AAAGAGTTTT	AAAGTGTGTCT	420
GGGCATAAGT	CTGCCAAGTC	CCCAGCTCCA	TGTGCCTTCC	TAAGCCCCGA	GGTTAGTAGT	480
GGGAACCAAA	CATCTCCACT	AGAACAGGGC	AACCGACAAG	ATTTCTTAAC	ATGAAAGGGC	540
TCGGTATGTA	AGAAATGAAG	TAAGTGAGTA	GTTTGGTGGA	TTAT		584

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

AGAATGAGTT	CTCTGTGTGG	AGATTACACC	AGCATCTGCG	TCCATTAATG	CAAACGTCAC	60
TTACAAGCAG	GAGTATCTGG	AAGGAGGATT	CTTGAGCTGA	AGTCCAATAA	GAACAGTTAA	120
TCCACATTT	GAGCTCTCTT	CCGAAGTCTG	AGGCCAGAGG	GAATGAATCC	GCCAAGATGT	180
TTTGATAGA	AAATAACAGA	AAATCCAATC	CGAACTGACG	CAAACAATAA	GGAGATTTTA	240
TTGACTCACT	TAACTGGAAA	GTCCAAAGGA	ATTAAGCTTC	AGGTGAGGGT	TGATCCAGTA	300
ACTTAATGAT	TTTGTTCTCG	GTATGGGATC	CTGTGTTACT	TGCCTATCAC	TGTGTAGCAA	360
ATCACTGGAA	ACTTAGTGGC	TTATAGCAAC	AAAGCCTTTT	GCTTATCTTA	CAGCCACGGT	420
GGGATAGGAT	TGAAGAGAGG	CTCAGCTTCT	GCTCTGGCTC	AGACTCTCTT	ATGAGGGTAC	480
AACAAACAAAG	GTGCCTTTG	GTGGTGTGAT	CATCTGAGAT	CCTGAGGACT	GGAAGGGATGT	540
GTTTCTGAAA	TGGTCCATTC	ACACAGC				567

948

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

TTATATATAT GGCTGTGCAA GTCCCTTCAT CCCTTGACAT GAAAGCAAGA AGGGAAGAAT	60
GTAGCCATGA TCATTGGGAT CAAGGTCAGG CCATGCTACT CACTTGCTGC ACATCTTGGG	120
AAATTACTTA ACTCCCTGAG CATCATGTCC TTTCCCTGTG TATTGCCGCC ACCTCATCTA	180
GCAATCCCAC TGCCAGGTAT GCGGCCAAAA GACACTAAAT CATTGTATCA AAGAGATAACC	240
TGCCCCACCA TGTTTGTGC AACGTTGTCC CCAATAGCCA AGATATGGAA TCAACCAAGA	300
TGCCCATTTGT AAGATGAATA AAGAAA	326

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AGTGGAGCAG CCAGGACACA AACTGGCACC CCCGTGGGAT GCTGGCGCCC CAGCGCTnTT	60
CCCGGCTGTT GCTTTCTTTA ACTGAAGAGT AGGAACGTGCA CACGTGTGTT GGGTACATGT	120
GCACATCGTG TCTTGCCTGTT ATTCTGTGGAG GTCAGGGTCT GAAGTCCTGG CAGACAGCCT	180
GGAGGGCGTG TCCCAGCTGG TGTGTGACAG GCCCCCAGGC GGATAGCAGT CTCTGTCCCTC	240
ACCGCTCAGC AAGACGCCCTG GCAGGGAGGG GCGGGCTGCC GCCCTCCTTG CTGGCTGGC	300
AGGTGGGTG AGGTCGCTCT GCGTGCCTGC CCGTCTCACCC CCTGCCTTG CCCCATGCAG	360
CGGACCGGCC CCGTCATCCT CGGCGCCAG CAGTGGGAGC TCAGACGACG CCATCCGCTC	420
CATCCTGCAG CAAGCCCCGC GGGAGATGGA GGCCCAGCAG GCCGCCCTGG AGCCCCCCGT	480
GAAGCCCACC CGCGCTGCCGC AGCCCGACCT CGCCCTGCTC ACCCCCCAAGC TGCTGTCTGC	540
CTCGCCCATG GCGGCCGCGT CCAGCTACGC TCCTCTCGCC ATCTCCCTAA AGAAGCCTCC	600
GGnGGCCCCC GAGGCGGGCGC TCGGCTC	627

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

AGATTTGAAG AnACACTACA GAGAAATTAT CATCAAAAGA GCCTGGTACC GGTACAAAAA	60
CAGACAGATT AATGGAACAG CATAGAACn CCAGAAATCC ATCCAAGCAT CTACAACCAA	120
CTTATCTTG AAAAACAGTT AAAAACAGnC TCTTCACAA ATGTTGCTGG GAAAACGTGGA	180
TAGCCACATC TAGAAATATG AAGCAAGACT CCTCCACCTT AAACAAAAAA TCCTCATTAA	240
ATGGATTAAA AACCTAAATT TGnGACCAAA TGCAATCAA TTATTAGGGA AAATGGGAGA	300
AACCCnGCAA GACATTGGTA TAGAAAAAAA TTCTTAGAAA AGACTCCAGA GGCACAATCA	360
CAGCCAAAC TGGCAAATGA GATnACATCA AATTGAGAAG AT	402

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

ACCCnTTTTT CATTCTGGG AAAAACTTAA GCCTGTAACA TTGAAGAAC CAGAGGAAGC	60
CAGTGAGATA GCACTAGTGA GAGTTGGAT GGGATGGAAG GTTAGCTGAA ACCTGGGGAC	120
GGAGGCGGCA CCCCTGTGGT TGGCCTGAGC GGGAAAGGTAT GGACCGACGTG GGGGGACGGA	180
AGTCGTACA GGGAGTAGGC GGGGCTGTGC GTTCTGTGT GCATCAGCGG TTGTTTGCT	240
GTGTGGAATG GGGATAGGGC ATATATTTTC CAGATTTGC TTTTGGACTT TGAGCTGTCT	300
GTTTCCATCA TGGGCATCGG GCCCGCAGTT AAAGAGCGCC AGACTCCGGC GGATGGGAAT	360
GGACCGTGCA CCCCAGCAAG TCTGGCTGAG TTCACCTGGA GACCTTAGTA GGCGGGGCTG	420
CCTTTCCAT GGCATTTGGT AGTTCCAAGT TTGACTAGTT AACCATTAAT TTTTATGGAG	480
CTTGTTCATG GGAAAGAATT TCATGTTGCT ATGGGAATGA CCATTGAATG CCGGCCCTGG	540
AAAACAGCTC AGGGGCCTTC TATCACCAGT CTATCATCTG TTAACGTGA CAGACACTGG	600

950

628

GGATCAAAGA AGTTATGGCA CCTACCCG

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

CATTAATCAT CCCACACTTC TGGGTTACAC CAACAGGCTC CCGTTGCACC ATCAAACAAGA	60
AAGCTATAAG GCAATCATCT CCAGTAGTAA CATTAATTCT AGGAAGCTTA CTCTGCTGAA	120
ATAAACAAAGT GAGTCAGAGG TGGGATGGGG AGAACCGCAC GGACCCAAGA CAGGAATCCA	180
CGTGGTCATG GCTGTGCTGT TGATCCAGCT GAGAAGTCAC GTGGACAGGG ACTGTGGCTG	240
TGACTATGGG TCTGACGAAG CAGCAGGACA GGAGGCAGGG GCTCTGAGCA TCCGTGTCCC	300
ACCCCAACTC ACATTCTACC CGACACTG	328

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

AAGAGTTCTT CCTCCCTTGT AGAAAGAACAA AAACCTGGTC CCCCCACAGG AATGGACACA	60
TAACAGCAAG GCCTGAGTGC TGGTCAGGAG ACATGGACCC AGGGAAAAGT TCCAACCGTG	120
GAACCCCTGGC CTGGGAGGCA GAGGCCAGCG GAAGGTTGGT TCTTTAAAGA CTCTGATAGT	180
ATGCACGCAA GATCATGTAC ACTGTGACTT AAATTCAAGG TTACCTTCTA TTGAGTCTGC	240
ACGCTAAAAA CAACAACAAT AATAATAAT GCAAAACTGAT TTGATGATAG CCTCGGAAAC	300
CCAGCGAGTG AAAAACCTA CTGGCAAACA CAGACTCTAA AACAAAGCAA AGCAACTGCC	360
AAGAGCCAGC TGCCCCAGCT TCAGGTGTGG CTGAGCCACA CATGGCTGTA AGCCACAGCA	420
CCGCCAGCCA GCCACAGGCC ATGAGTATCT GCCGCCGnCT TCTCCCTCTG CCCCTCTCCG	480
CTTCCGT	487

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GTGAAGTCAT GGACCCAGT AGGCCTATTG CCCTGTGGAT GAGTGTCTTC TGTGGGGTC	60
TTCAATGTTT TGGCACTCTG TGCACTGTGG TCGGTCCATG ATGGCAGGGA ATCGGCTCGC	120
TTTCTTCAC AGCCCCCAA GCACCTACCG CAGGGTGGGA ACTTCCAGCC AGCCCAGGCC	180
ACATTCGGCC AGCAAAAGCA TTTGGTTTGG CTCTGCCAAG GGCAGCCACA GGCAGGGACT	240
CAAAAGTCAG TAACTCTCTA GCAAGCTAAT TTTTAAGTTG ATAATTTGT ATGGCCCACA	300
AATGATGTTA TAAATATCCC AATGCCCTC GGCAGAAAAA AAAAAGATTT CCCCACCCCT	360
GCATAGCTGA AGTCCTAAGT TGTACTTGGC CAAATGCGCT CTGCCTGCC AGGAAGGAGT	420
CCTTGGATGT CCTGTATGTC GCTGGCATGG GCACTGAGGG AGCAGCAGC	469

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TTTTAAAATG CTTTGTGGAA GTCACAATCT AGTTGGGGAA GTGTCGAGTT CATGCCTTTC	60
CTTTTAAAAA GATTTAAAAA GAAGAAATTG AAATTCCATC ATTTGAAAAA GAAAATATTT	120
AAAAAGAGAT TTAAAAAGAG GTTAAAAGAG GGAAGATTTT TCCCTTACCT CTCCCTCCTT	180
TTAATATAAT ATCCAAAATA TTAAAATATA TTATGATATA AGCATTATA TTATTGTCTT	240
CATATCTAAT TTTTTCTTC TTTAACGTTG TTTCCCTCAG TAACTCAGAC CTTTTCTGAG	300
TTTAAATTTT CAATAATAAG AAATGAAGGA ACTTGTCAAGA TGTTGCTAGT CAGGAAGGCT	360
GCCATCAGGA CTCTGCTGGA AACTACCTTT CCCCATGCAA ATGATTGAG ATATTGATAG	420
CATTAATTTT TTTCAGAAGG TACnTATATA GAATCCCATT ATTCAAAAGG	470

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs

952

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

ATACCACGTG GATCCAGCAA AGTGCTTCTG CAGAGCCAGT CTGACCTGGG GCTGGCCGGC	60
TGCTTCCTCT GGCTGGGCAT GGCCAGACCC GCTCCTGGAA AACCCCGAGA CATCAGAGGG	120
AGCCTGGGGG GCCCCGCAGA GGGAGGCGGC CCAGCGCTGA CTCCAGGGAG ACCCCCCCAC	180
ACCCCCACAG CGGGCTCAGG GCAGGGCCT CGCTGAGGAG CCCAAGTGCT GCCCTCTAGG	240
GGTGACCTTG CAGCTTCCGG GGCCAACCTG ACTGCAAACA GAAGCAGCAA AGTGCACAGT	300
CCCTGAnCCC CCAGACTTCG AGACAACACC CGCTGTGCCCT GTGCCAAGAT GAGGGTGCGC	360
CGGCATGGCT GAGATGCGTG GGGCGGCTC TCCACCCCTG TTCATCTCTC TCCTCTTCAT	420
TGCAAATCCT GCTTCAAGAG CAGACCAGAG GGCAGGCATT TGGCACAGAG TTAAACTCTG	480
AG	482

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GGACCGACAG TGCGCACGGA GGCCAGGTCA CCCCTCTCTG TGTTCAG ACACATTACAA	60
GACCCCTCGGA ACAACCCCTGA CAGCAAAGGC GCTGCAGGAG CTCTTCGCA GATGAGAAC	120
CTGAGTCGGG CAGAGCTAGT AAAGGCCAGG ATTGGCCCC AGGCCCTTG GAGCCAGAGG	180
GCCTAGCATT TCCCTTCCTC AAGCCATCCT AGAATGCTCG GAAGCAGAAC CCGACCGCAA	240
GCTGATAAGG GAACCTGTCA CGCATAGCGG GAGCGTCCCC GAGATCTGAG CTGTGGTCCT	300
CAGGGGATGG GCCTGCGTCA TCGGCCACCA CTGCCGTCAAG CATGCCGCC GGTGTGAGGA	360
GCAGAAGGCTG TGACGGGAAG GACTAACGGG AGTGAAGGAT TACTCAGATT GGAnTGTCCC	420
TGTTCGGGG TTAGTCCAGG ATCAAAGGAC GGGAAAAAT GGGACC	466

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

TGAATTCCCTA AAAACAGGAT GTTAGGATGC CTTGGTTTT CTAAACAGAC AGAACACTGT	60
TCCCCCTGTTT TAAGTATATT TGGGAAGGGG TGAAGGGAGG TGGAAGGGGA GAGGCAGTCT	120
AGTATACTTA TTTCAAGAGC AAACACAGTC TGATGAATGC CTTGGATTGT TCTTGATGCC	180
AGCTGACTTT TCAGCACTCA TTAATGGCTT CCGTGTGTGC ACAGTCTTCC AAAGGCATGG	240
AGAGAAACCA TCATGCACCT AACCTCCATG GCATTGCTGT GTGGTATCCG GGCCCAATGT	300
CCCCACCCCA TTCCAGTGTG TCCTCATTTG TAAGTGTGGG AAAGAGCACA GAGAAACCAT	360
CATATCAAAT CAGAGCTGGT GTTTATCGAA CCCCCATAAT GTCAGGCAGT AGACA	415

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GGCACACCTT TTAAAATGTG ACAAGCGCTC ACACAGCAGC TTGCGGGTGC CAGGCCAGCT	60
CTAAGCTCAG GAGCATCAC ACCGTAACGA TGGTACCCAC ACCACATCAC CAGCACACCA	120
CGGCCGCCGC ACACAGTGGG CACCCGGGCC AGCGGCACGC CTTACCATTG CTCATGCACC	180
CGCATTACT CGCAGCAACG GCCTAGCGAG CGGGGGTCTA TTCTTAGCCT CACTCTGCAG	240
GCGAGGAAAC AAGGCCAACG CCTTGGAAAGC TTGTCCCTGGA GGAGAGCCAC GCGGGAAGTC	300
CTGCAGCCTC TGGCCACTGG GACCCAGCTG CCCGGGGCGG CAGACACCCT GGGAGGGAGC	360
TGCATCCTGC CGGCCCTCCC CTTCCCTGAGG CAGGCCTGCA nTTCCCTGTTG CGCCTG	416

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

AAAAGCACAG ATACTTTTC CTGAGCTGAG AGCACTGTGA AGTCCCACAT CCATAACGGG	60
CAACCCCTCC TGTGAGAAC CTTCTGTGGA GCTCTGAAAA GAGAACTGTC AAGGGCAAGG	120
AGGCTTGTGTT GGTGAACCAG GAGTCCTAAG CTTTGCTCTT TGCTCTGTCT AGCAAGTTTT	180
CAGTTACCTG CAGCCATTTC TGGGTTAGGC TCTTTCAAT AGTCACTTCC ATGGTTTAAG	240
TAGGACATAG TTCCTGAAC CAAGCAGACA CTTAAAGTTT AAACCCAGG GTCTTATGGT	300
ACTAGTGCAG AGAGAGTGAA AAATGGGCCT CATAGACGAT CCTTAGTTCA CTGAGACACA	360
CCCTTAGAnG GTAGCTCTCA TGAGTTGAGT TGGGTCGAAC TCTTGCTTCT GGGCTGCCAT	420
GTGACTATCC TCTGTCTGTT CATnCTGGT CTCACCAGAC AGGCAAACCA AGGGGCCTGA	480
CCAGTTGGGA GGGTCTACTC CAAATAAACAA AACCTCC	517

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

TTCCCTTGTT ACCTGTGACA TGGATACAGT GCTTGCAAA CTGGATAACT GAGGCCATGG	60
CCTCTGAGAG GACAGAAACA GGCCCCACCA GCTCAGGGCC CTGCCAACCT GACTCTTCAT	120
CTGGTGACTT GATGATGCAT CCATCTCAGG CTCCAATCCA ATGAGAAGCA CTAGTGTCCA	180
GATCCTAACCC ACAAGACTAC TGCTGTCCTT TTATGGGCTT CCCAAACCTG TGTGCTTGTC	240
CAGAGCAGCC CACCCAGCTG CTTTGTGACC TTCCCTGGAGT GGCGGCACCA CCATTTTGAG	300
TGCACCGTGT GCGAAAACAA AAACAACAAC AAAAAGCAGA AGGC	344

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TTGGCTTTCT CCTTCCGCCT GCCTGGAATG TGGCTGTGGT GCCTGACCCG GCTGCAGCAG	60
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955

TTTTGCAACC GGATGGAGGG TAAGGAGCCC AGAGCAGATG TTAGAAGGAG CCTGGCTTCC	120
CGGTACTGGG TCCCAGCTAC CACATCGGCC CTGGGCTGCC TGTTCCCTTT TGTTTGTTTG	180
TTTAAAAATT TATTTATTTG GAAGGCAGAG TTAGGGAGAC AGAGATCTGC CATTTGCTGT	240
TTCGGTCCCC AAATGGCCAT TAACAGCCGC GGCTGGGTCA GCCCGAAGTC AGGGGCCTGG	300
GGCCCAAGGA CTTGGGCCAT CTTCTGTTGA TTTCCCAGGC ACATCACTGG GGAGCTGGAT	360
GGAAGTGGAG CGCTGGGACT CGAACCGACG CCGCCATCGC ATGGTGGCAT AACCCGCTGT	420
GCCACAGCGC CAGCCTTCCC GCACCGCCTG TTGGTCCAGG TCCTGGCTGC CAGGAGGGAG	480
GC GGTTTC	487

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

AGGAAACAGG AGACAGGGTG CCTGGCTTT GGCCTGCC ACTGCTCCAC GACACGGGGC	60
AGCTCACCCC CTGGTCCAGC CTGGTTTCGG GAGCGGTGCC TGGAGCAGAG TGCCCGGGGA	120
GAGGCCTGAG CTGAGGAGGC GGACAGGGCC AGGACGCGGA GGGCCTCCCT TTGTTCCATC	180
GCCTGCCAAG CAGGAAGGCT CTCCCCAGGT GATGCGCCCTT CTCTGGGCC GCTCCCTCC	240
TGGGATTTCGT CACAGCAACC TGAGTCTCAG GGAGTGTGCG TTAATTATCA AACGCTTCAC	300
AAGCATCAGG AGCCCGCAAG GTGCTTCACC ACCATAAACG ATTTCCTCTC ATTAGTGTTC	360
ATGATCATAA AGCTTCAGAT GCGGCTCCCA TGGCAACCTT AACTCCTCTC CTCCCCCCTC	420
ACACACACAC ACACACACAC ACACACACAC ACACACAAAC ACACAGTGAC AGGATTTTC	480
ATTGCAGTAA TAACTGCAGC TCGTAAACCT GCCAAATTAT GGGGAAACAT TTATTTTTAT	540
AAGCTGAGAT AAGTAGGCAG CGCGGGGTA GCAGATCCTC GCCTTGGTGG CTCCAGAACAA	600
AGCTGGTCCT CAGACTAAAG ACATTCGCAA G	631

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CATTTGCATA TATGCTAAAG CGATTTGTTT TGTGCTAACC ATGAGACTTG TATAACAGTC	60
ATAGTATACT ATTTTAGTA CTTCTTGTAG CTTTAGTTAA TTGTGATCAT TCTGATATTT	120
AACTTTTCAT GCTGGGGATA CATCTAGGTA TTTCCTTTG GTATTTCCAG CGCATTTC	180
TCACCCCTCAA TCATTAGGAA GGATCCGGAC TTACAAGATA AAGCAGTGAG CAGCACTCAG	240
AAGCCATGTG CTATTAATTA GAGTGGCTCC ACAGCGATGG AACCCATCCC ATTGCAGGCT	300
GGCTTGCCAC GGCCATTCTC CTTCTTCGAC CTCTGTGCCA CCAACTATCC TGACACTCTG	360
ACCTGCGGAT TTACTCCTTC GTGTCCCACA ACCTGTAAA GAGATAGGGA TGAGCTCCAG	420
AGCAATGTTT TATGTATCAA TGGTGCTACT ACATCCAAA TTCTTGACT TGAGCTCCAG	480
CAATATGAAG TACTTTTCG AGTGTTCCTA CACAGTAGAT TTATTCATT AGCTACTCTA	540
A	541

(2) INFORMATION FOR SEQ ID NO: 392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

ATTTTAAGGA AGAATCAAAA TGAAATGAAG AAACATAGTAG AACAGGAAAA TGTGATAGTG	60
AAGAGAAATC AAAATGAAAT GAAGAGCTCA ATAGATCAA TGACAAATAC ATTAGAGAGC	120
CTTAAAAACA GAATGGGTGA AGCAGAAGAG AGAATATCGG GACTTAAAG ACAGAGCACA	180
GGGAAAACAT ACAGTCAAAC CAAAGAAAGG GAAGAGGAAA TTAGAAATCT AAACATATTG	240
TTGGGAATC TACAGGGATA CTATTTAAA AACCAACATT CGAGTTCTAG GGAGTTCCCTG	300
AAGGCATGGG AGAGAGAGAA AGGCTTAGAA GGCCTTTTA ATGAGATACT AGCAGAGAAC	360
TTTCCAGGTT TGGGAGAAGG ACAGAGACAT CCTACTACAG GGAAGCTCAT AGAACCCCCA	420
GTAAACCTGG ACCCAAAAGA GATCCTCACC ACGGACACGT GGTAATTAA ACTTACCACA	480
GTGGAACAnT AAAGGAAAAG ATCCTAAAAT GTGCCAGAGA GGAAAnGGCC	530

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

ATTC AATC CCT GTTA nTTT CT TCTG AT TT TCAT TnTT TC TCTC CCTA CTAG AT TT GG	60
GATT GGTT TG CTGC AGTT TT TCTAGG CCT TGAG ATGT GC TGAA AGTC AT TT ATTG GT TA	120
CCTT CCAAT TTCTTG ATAT ATGC nCCTAT TGCTATAAAC TTGCCTCTCA GTACTGCTTT	180
TGCTGTATCC CATAAGTTT GATATGTT	208

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

GCCA ATCCC CCGCCCAAAG CGGA ATATAA CTCATGACAT CTGCAAATAC ATTTACAATG	60
CCCAGCAACG CATTAATTAC GTTTTCATA CTGTCTGCAA CACTCTGCCG CACACTCACC	120
CGATAATTCA CAAAGATAAA ATT CAGCACA AAACCCGCTA TTATAGACCC GACAATCATG	180
CCGGCAAGC	189

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

CTCACCCATT TGTGCAGATG CTCCTCAGTG CTCTACTCTT CACCACCTGA GTTCACTGCA	60
TTCCCTAGGA AAAACTCAAAT ATGCAAATAT TAGCCTCTCC TTGTAGTAAA ATGATTGCAT	120
CTCATGTCTT GTGTGAGGTG TGAGGACCAAG GCCATGTCCT AGGGGTTTTT CATCCCTGCA	180
GCCAAGTGCC TTGGGTATGT TCAGTTGCA TTCCCCAAA AAGTAGTTCA GAAAGTATGT	240
TTCTCCCCAA AATAAAGTC AACTGATGT TGATTATATAA AGATTTACTT ATTTATTTG	300

958

TTTGTTCCTT TTTTTTATT TGAAAGACAA ACTGGCTGCA GCAGTCAGAG CTGGGCCAGG	360
ATAAAGCCAG GATCCAAGAA CTCCATCTGG ATATCCCAG CAGCTGACAG AACTCAAAT	420
ACTTGAGTCA TTATCCACTG CTTACTAGGC ATGTTAGCAA AGTGTAGAT TGAATGCGGA	480
GTAAGCAGGG ACTCAAACCA GCACTCATAT ATGGGTACAG GGGCCCCAGA GTGTCAGCTT	540
AACCCATTGn ACnATACTCA CCCCCCTATG GGGACTCTAA AACAT	585

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

GTAGCAAAAA TATACCACCT GCAGTTCCAA TTATCTTGCT AGAATTATAT GTTTGACAAA	60
CAATACATTA ATTATAACCA TTTTTATCAA TTTTACAAGT GTCACTAAC CAGTTATTTG	120
TATCACTTTG TTCCGTGATG AATTATGGAA AGTAAGCCCT TTAATTTTTA AGCATTTTAT	180
CAAAGTACAA TATACATCCC AAGAAATGCA CGTGAGGTAC AAATGAATGA GGTTTTGCC	240
ATCTGATCAC ACTCATATCC ACCACTCAAA CTAAGAAAGG GTTAATGATA CCTCGAGAGT	300
TCTAACTATT CTCCACATTT CTATTGTTT GAACATGTGA AAGTGTATCA TCATGTATGT	360
GGTATGATTC AGTGAACAC AATTATAAC TATATTCAA ATTATACGAC ATCCACATAG	420
TATTTATACT CTCTATATTC ACTATTAAAA ACAAGAATGC ATGTGGTATT TTTCTTTAG	480
GGTAAGACTT ATTCACTTA GAATAATGGT CTCCAGTTGC ATCCATTCA CTTAAATGT	540
CAGGATTTCAGA TTCTTTACA GCTGAGTAGC ATTCCATCAT G	581

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GTCAGAAAAA TAATCAAAGG CATAAAATT GGAAAAAAAG ATGACAAAAA TATTCCTATT	60
TTAAGATAAC ATAATTCTTT ATTTGAGGAA TCAAAACTC CACTATTAGA ATTCAAAAC	120

959

AAAATTTGAT AAAATTTAG GATACAAAT CAACTTACAA AAATCAGTAA CATTCTTATA	180
CACTTACAGT GCTCTGGTTG ACAAAAGAAGT TACAAGTTCA GTCTCATTCA CAGTCATTAC	240
AAAGCAATTA AATACCTTGG GATCAATTAA GCAAAGGATG TGAAAGCTCT CCACAACTGA	300
AATTACAAAA TGTTAATGAA AATTATAAAA GAGACACAAC AAAATAGAAA CATTTCAT	360
GATCATGGAT TGTAAGAAC TC AGCTTATCA AAATGTCCAT ACTACCCAAA GCAATTGCA	420
GATTCAATGT GGTTCCAATC AAAACACAAA GGnAATTCTT CAAATATCTA GAAAAAAATA	480
CTAATGTTCA TATGGnAACAA GAAAACACCC TGGnAAACAA AAGCAATTCT AAAAAATTAA	540
AACAAAGCCA AAGGGTCACA ATACCAAATT TAAAGCATA CTATAGGGC TGTTATAATC	600
CAAACAGTCT GGnTCTG	617

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

TGCTTTACTG CTACCAGACAA GTGGGGTGTT TTCCCTTCCTG CTGCACAGAA TTTTTACAGG	60
GATTTAGCAT TTCTAAACG GTATTCATA AAGCCTTAAC CGATTTCCCA CAAAATAGAA	120
CTGGGTCTTA GATTTTCACC TTCATTTAGA AATCCAGTCT ATCAGGATCA ATTTTACAC	180
TTTTTAAATC ATTTTAGAAA GATACACACT TGCCTCCCAG TCATCGTGCT ATAGGAAAGA	240
TGACACTGGG GCTGATTTG ATGTCCTCCCT GAGTGGCTTT TCTTCTCATG ACCTTAAAGC	300
TGCTAACAGC AGTCAATAAT TGAGGAGAGG TAGGCCAT TATTTTTCT ATTAAAGG	360
CAAAATTAA GCTACTTATA CACTGCCATT TGTGCTCTAT CTCTGAAC TG ATAACCTACT	420
CTAGTGTAC AGCAGTCTAC CAAAGAGGG AATCCAGGG CCTCAATTCTT CTCTTGACAC	480
TACACG	486

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

ACAGGCCCTA TCCTATGGCT TTTCCTTCTG CATCTCTTCT AAGACAGGCT AACGGGGACA	60
CAGATGCCTC CTGGGCAGCC AATCCAATCA GGAAACCAAT CCAGAAGTTA ATGTGAAGGA	120
CAGTGAAACC TCAGGCATTG GTTCAGGAGT TACGGAATTT GTGATAGTTT TAGAACCTGG	180
GAAATAATTT TCTATGTGGT CTCAAGAAAA CTCACTTTCT ATTACAGAT AATTCTCCTC	240
CTCCTCCTCC CCCTTCTCCT CTTCCCTCTT CTTCTTTCTC TTATTAAAAA AAATAACATT	300
TATTCAAAG GAAGAGTTAC AGAGAGGGAG ACAGAGACAG AGTCTCTGCA GTAGCTGGGG	360
ATGGTCCAGG CGAACAGnGA GCCTGGAACt CTATTTGAGT CTCCTACGTG GGAGCAGGGC	420
CCAAGTACTG GGGCCATCCT CCCCTGCTTT CCCGGCACAT TAGCCAGTAA CTGCACTGGA	480
AGTGCAGCAGC TGGGTCTCCA ACTACACTCA TACTGGATGC CGGCATTGCA AGTGCAGCAGCT	540
TAGGCTGCTG CACCACAGGT GGTTCTAAA TTTCATTTC AATATATGTT CTGAAATTTT	600
AACACATAAT TGTACTTGT TATAGGATAC ACTACAGTAT TTAAATACAT GTATTACACGT	660
 GTAATG	666

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

AGTTCTTCCC GAGACACAAT TCCTCATGCT GGCGTTTG TCTTGCCTTT CTTACCTTCC	60
TCCTCTAGGA ATGAGGAGAA AAGAGGGCAC TGAGAGAGAG GGTGAGAATA ATCGCTCTTT	120
TCCTCCCCCC CTCTGAGCGT GTGCTCTCTC TGAGGCTCAT TTCAATGGGT TGGGAGTATG	180
GGGAGAAGGG GTGGCAGGAA CAGAGGGTCC CGTGTGATCA CAAGAGCATG CACTGTTTCC	240
ACAATTATTC TAAGTTCACT AACTACACAG CGTGGCTATA TGTTTCATTG TGCCTGTCTC	300
TGAGTGCCTA GAGAGCTGGC CACACGTTAT TCTGGGTATG TCTGTGACGA TGTCTCTGGA	360
TGCCATTACC ACACAGAAGG TAAACTGTAA ATGCATGCC TCCCCAGAGT GGTGGCTCC	420
GGCAATCTGC TGAAGGCCTG AACAGAACAA ACAGCAGAGT GAGGCGATCT ACTGCCTCTG	480
 CCCGG	485

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACATTCTCA	AAACTAGCAT	CTGAATTATG	GGAAAAGACT	TTTTTCTCAC	CTTAGCTAGA	60
TTAATGCAGA	CAGAAAATCG	GTTTAATATT	TGTGTGGACT	AGGGGTGGTG	TCTGTGTGGT	120
GTTTAAGTGA	GGCATGTGTC	CCATATTGGA	GAGGCTTTT	CAAACACAGG	CTACTCTGTC	180
TCCAATCCAT	TTTCCTGCTA	AAGTGAACTA	TGGGAGGAGG	CAGATGATGG	CTCAAGTATG	240
TGGATCTCTG	TCACCCATGT	GGGAGACCTG	TAATGAGTTC	TGGGATCCTG	TCTTCAGCAT	300
AATATAATCT	TGACTGTTGG	GGGCATTAG	GGAATAAGCC	AGCAGATAGA	GATCTGTTAT	360
CTATCTATCT	ATCTATTTGT	GTTTCTGTAA	TTCAAATAAA	AATGGAAATA	AAATCAAAAT	420
GAAGATAAAC	ATTTGTGTTT	ATAATAGTTT	ATTCAAGATG	ATTAAATTCT	AGTGTACTGG	480
ACCACTATCA	CTTGCAAAAC	ATGAGAACAC	TGTGGATGGT	AAAATCCTCT	TGCTATTCTT	540
ATGTGAAGAG	TTAGACTGCA	CTT				563

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

CATCACTTTA	AGTTGAAGGT	ACAACCTCAT	GTGAAACTCA	TGAATTCTTT	GAAAATGTAA	60
TGTGGCTCAC	ATGGAATGTT	CAGCGTGCCA	TGCTGCCCTC	TTACACTTGG	AAACAAATGA	120
AGAGAGATGA	CCAATTCTCA	TGTGACAGTG	ATGGAGCCCA	ATTATGGATG	ACTACCATGA	180
TATTCTTTG	AAGAGTCACT	TGAGCTAATG	AATTAATATA	TTAATTATA	TTGTTAATTT	240
TAACATCTA	ACACAGTTAC	TATTTATGTA	TGTATGAACC	ATAATATAAT	AATTTAAGGn	300
ATTTCCACAA	ACAATGTA	CT ATATTAGTAG	AGAGTAAC	AACTTCTCT	TTGCnTTATA	360
TAATTATAAA	GGATGTCAGA	ATGATACATT	TTCCAAAACA	ACATATACTA	TAATATTAGG	420
ATAAAAATAAT	GGAGTTAA	TT				440

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

ACCAAnTGACG TTTTAGGnGA CACTTATCA CCTTCTTACA CCCTAGATCA TCTACTTACC	60
TACTGTGGCT GCATGCCTAT GCCCTTACCA TGGCATTTC ATCACCAAGGT TAAAAAACAGC	120
AGTTCTCAA TTCCATGTCC CTCTACCATC AnnCATCACC TAGGAACCTTG CTAGAAATGC	180
AAGATTTGGG ATCCACGTTG TGACACAGTG GGTTAAACCA GATCTGCAAT GCCAATATCC	240
CATGTGAGCA CTCGTTnAAA TCCTTGACTG CTCCACTTCT GATCCAnCTC CCTGCCAGTA	300

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

TTATAAATAA TAATAATAAA AAAGTGTGCA CAGCACAAAA GAGAGAAATG nTTCAGGGAT	60
TCAGAAGCTA GAAATTCACT TCCAGGGThA nTGGGCCTTG GCCTCAGAGG TTTTGATTTG	120
GGTGTAAAGTT GATGCTGCnA GTCCTGGAAA ATTTGGGATG nnACTCCGCA nTGTGTATG	180
TATTGTAAGA ATATACACAA TCTTAAAAAA GAAAACAAAC AAACCAGAAA AACCCCTCTC	240
GnCTCAGTAA CTATATTAC CCTGAGCCAA GTGCAATACC TGGCTCCAAG AAGATTTAAT	300
AAATCTTGTG TCTTAGGCCAG ATCCCTTCAG TTAGCATAGC TATCTCTAGG ACAAAATCT	360
GGTGAAAAAG AGAAAATGTA ACAAnTGACA AGTCAGTAAA ATCACACTTA GCCTGCCAA	420
ACCCTTGACA GGCnTGTGA	439

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

AGGGCAATCA CTTAGATGCA ATGACAAGGn CAATATGAAC TCCAAGAAAA CAAAAATGTA	60
AAGTCTCTCT ACCATTCTTA CATACTCAGC ACAAAAGTATA TATTCAATGA CTAAGGCAAC	120
ATTTAAGAAT GAAGGCGTAG TAGTTAAAAA AAAATAAAA CAAAGAATGT AACCCATACTT	180
ACCAAAACCT AGGTTTAAAT ATAGTGGATT ATATACATTTC AAATATAGAT AGGTATTTTT	240
TAATTACTGA AATCATTAAAT AAAGAGAGTG GCAAAAGTAT ACCATTAAAC TTCTCTTAAG	300
AGCGGTATCC ACTGTGTTA TCCTTATAAT TTAAAGTTAA AATTCTGAGA GGACTCCTGA	360
TnCAGAGGAG GCATCAGATA TCAAGTCAGG TTAACACAAA TGnCACTTT	409

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AAATTGTTTT GTACAAAAAA TATTTTCATT TCATTTCCA CATGACTTTT GAAGTACCTG	60
ACATACTACC CTGTACTCTT TCAGGACATT CTAGGCCTAA TAGGTTGCCCT TTAATTCAATT	120
TAAAGTATTAA ATTAAATTA TTTCTCCCCT TTCACATATG AGAAAAGTGA GGCAATGAATA	180
GAGACTCATC CAAGATCATC CACTAAGTCA CTCTATGTGG TGGAATGAGA AGGCCATGCA	240
CAGATGGCAC TGGCAAACAA GTGTCAGTTA CTCAGGAAAT GGCTTGGAA CCCACCTGGC	300
AAAGGGGCCT GCCTGGCAAC AGCnTnGATT GGTTAGGGCA TAAACCTCCC CTTGACCAGA	360
TTGGCTGCCT GGCTATATAA GCTGCTGCAC CAACTGAAAT AAATGAGTCT GCAAGCTGCT	420
CACCTTGGC CCGCTTCAC CTGACTCCTG GTGTCTGTGT CATGACTCCA TGCCTCTTGC	480
CTGCACGTGCA CTCCCTCTCT CAGAATGAGT CCACACAAAC ATCTCTAACCA GTGTTACCCA	540
GAGTCCACCC CCTCTTCCAA GGCTTCAG	568

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

AGCTGTCTCC ATCCTACTTC AGGAGCAAAT GCTTTGTCCT CATGCAAAAA GCGCATACTA	60
TGATTTTACA CCTGGGATCT TCATCACGAT GTACGTGCAC AAATGTGCAC AGGACAACCTT	120
TGTTTTACA TTTTGACTCA CTTTCTAAAA ATGTAGGCTA ATAAAATTTG TTGATAACTA	180
CAAAACTCTC CAATCACACCA CACCCCAAAG CGCCTTCAAA TTTTCCAAAC TGAAATCTA	240
CAAGGTATCA ATATTACAAG AAGTACCTTC ATGGATGTCC ACTGAAATAA AGTCTCACTA	300
TTGTGCTTTC GGTCCCTCCAT TTTCCACATC TGTATAAAAA AAATCACACC TCGCTCTATA	360
ATTGAGTTTC AGAAATAAAG CTCTACTACA TGCATGTGCG TTCATACCAT TTCTATAAAA	420
ACCAAGGGCT CAGATGCCCT TGCACAGTGA AACAGATCAC AGTGAACAG ATGATGGCAG	480
GCACATACTC TTCTCCTTGC TTCTCAGCTC CTCCTTGCTT GAGAGAAGGC AGGAAAGCAA	540
GCTGAGGGCA CTGCCATGTA TGAGGACCAA CCACTGTTTT AGTCCCTTTA CATGTGTTGT	600
TCTTATTTAA CACCTACAAC AGACCGAGGG AATCA	635

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

AACATCCGTA CCACTTGCC TCAGGTAGAA GCTAACACACA AAAAGAAATG CAGCAACATG	60
AAAATGAAAT GAATACCA AATAGACTGA CGCTTGCTG AAACCTGTTT GTGCTACCCCT	120
AAAAGGAGAC TAGAGAAGGC TAGAGAGCCT TGAAGAAAAA ATAAGAAGCA AAGACTTCAT	180
TTTGGACCTA ATCGGAAGAC TGGAAAGACA ATTAAAAGAG GACTGCACTT CTGAGTGT	240
CAGTCGGACT TGCAGTCCC TCCATGTTCT GTCTAAGATT GTCTTGAA GTGTGTTGG	300
CCTAGTGGTT AAGATGCCCTG AATTCCGTG CAGAGCnCTG GGTTCTCATG CTGGCTCTGG	360
TCTTGATTTT GGCTTCCTGC TAATACGCTT CAGGGGAGGC GGTGAGCAAT GGTCCAAGTA	420
CTTGGGGTCC TTTTACCTAT GGATTGAGTT CCTGATTCCCT AAGTTCACTT CAGCCTGGCC	480
CAGCCCTGGC TATTGGATGT ATCTGGAGAG TGACCAAAGG GATTGTATCT TAGTTTGCT	540
GTCTCTTCA CAAAGATTAATTC	564

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

GGAATATTCT GATCATTAG AACAAATTGA CTTGATAAAT TTCAATTGTA TTATTACCTT	60
CTAAATCAAA TAATAGTATA TATGTTACA AAACAGTATT GATTCTCTT AGTGAGTTCT	120
ACAAAATGCT AAATTCCTT TTAAATTAAA AATATTTGGT TGGTAGAGGA TGGCACTTGG	180
TCATGAAGCT AAGACACCAG TTGGAATGCC CACATGTCAT AGCCTGTGTT GGACTCCCTG	240
CCCTGCTCCT GATCCCAGCT TCCTGCCAGT GTGAATCCTG GGAGGCAGCA GGTGCTGGTT	300
CAAGTGGTTG GGCTTCTGCT GCCCACATGG GAGATCTGGA TGGAGTTCCC GCCTCCTGGC	360
TTCAGCCCTG GATATTGCAG GAATTGGAGA ACTGAAGCAA TGGACAGAAG ATAGCCCTC	420
TCTTTCTCCA TCATTCAGCC TTTCAAAGAA ATAAGATAAA CTTTTTTTA AACTTTTATT	480
TAGTAAATAT AATTTTCCAA AGTACAGTTT ATGGATTACA ATGGCTnGnC CCCGCCATAA	540
TTTCCCCCT ACCTnCACCC CTACCATCTC CCGCGCCCTC TCCCTCTCCC ATTCCATTCA	600
CATCAAGATT CATTCTCAAT TATCTTAATA TATAChA	637

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

AGGACTTGAA GCTGATCTAG AAAGTGGCT CTGCCTAGAC AGCAGTAGCA GCCCTGTAAC	60
AGGCGTCTGC CGGAAAAGCA CCAGGGCTTC TGCCCGGCTC CTCCTGAGGT GGGCTTTCCC	120
TACTTCTTCC TCTGCGGTT TCCTGAGTT TCCCACGGTT TCCAAGCTGC CTTGGTTGGT	180
CGTTCTTGT ATCTTTCTTG AAGGACCATC CTCAAATGCA GCTAGATCTC AAGTTAACAG	240
CCAGGCCAGG GTGGGTGGGG TGTCACATTG CTCCTCTGAG CACAGACCCC AGTCCCCCCC	300
TCAGTTACA GTGCCGTTTG CCTCATCTGG GCTTTGCCAC TCACTAGCTG TGGGACTTGC	360

966

CATGAGTTGC TTAACCTTTC TGTGTTCCC TCGTCTCAGC TATAAAAGGA AGCTAATAAC	420
CACCGCCACC TCCAGGATTC TGGGAGGCCT TAGTGAAAGC TAGGGAGAGC CGGGCGCTCC	480
GGCGGT	486

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

AGGATTGTT TGCTTATGCA AGGAAGGCCT TTGAAGATGT TTGTCAAACCT CTCTGTGATC	60
TGATGCTCTA AGTTGCTCTG ATGCGGACAT GTATTAGCAG CACATGTGTC TGCGTGTGTC	120
TGTTCTTAAT GTAGTCACCG ACAGCCTAAA TGCTTCTAAC GCCAGCTCAC GGGCACACTC	180
TTAATTGGTC ACTGTCCTTA AATACCCAGA GTTCCTACAA CCACGGCCAC ACCTCCTGGG	240
AACTAAGAGG GCTGTTGGCA ATGCACAGGA AGGAGGTCCA ACTGGGGCCG GGGCTCATGT	300
CCCCATCGAA GGAAGGACCC TGACTGCGTT GCAACTGCAA AGCCTTAAG AACTGTTTCT	360
TTTTTATTATT TGTGCCTTTC TGGCCTCATTT AATGAAAGAG CAGCTCAAGA TTCAGGG	417

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

ATAGGCATGT ATACATATGC ATCACACACA TACAGATGCA TCGCAGGCAT CCATATAGAT	60
GCAAAGTATG TTTCTGCATG TGTATATATG AGTTTACACA TGTTTGTGAA TGTATTACCT	120
GGATTTCCTCT ATATAATCCA GGGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTTTTCATTT	180
CTCACCCCTGA ATCTGGAACA GTGTCTCCTT GGCTAAGAAA AAAAATCACA AGGCTCAGAA	240
GGAGCAGATA AGGGATTCTC CAGAAATCCC CATCCCTCAC CTGGGAGCAA CATTCCCTAT	300
TGACTTGAAA GGTAAAACAA TCAGTTCCA CCTCATCCTC CATCCTCTGT GTGTCTGAAT	360
CATATTTTTT CTCTGGGGAG AAGTGTTCCT GAGACTACAG AAAACTCCCT GGAGGACAGG	420

967

AAGACAGAGG AAAGACCTCT GTGGGTTGAA GAGGCAATTG CAGGAAGCCC AAGTGGGAGA	480
G	481

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

TTATAAACTC TAAACATGTG CTCCCACAAG TACTGTTATT TCTCCAAGGC ATCACATTTC	60
CTGGTGGTGG CTTCTGGTTT AACAGTCTGT GTCTTACACT CGAGCAGAAA CCCTGTGAAG	120
CCAAGGAGTT AAAATCTTC ACCATCCCCT GCTATAGTAA AATATGGGCA TGTATATTGC	180
ACTTCACAAA TAATTGAGGG GGGGGGGAGT TGTTACACAT GAATGAGTAA CAATTCAAGGT	240
GGTCCAACTC TATAGTTAAT TTTTGATATA GTTAATTAAT TGATATAACT CCCTCAATTG	300
GAATGAAATC TTTCAGCAGA GAGATGATCA TCATCATCAA AATCTCTCT GGGTCCCACA	360
TGCCTACACT CCATTGAGTT AAGAGAAAGA TACTATGGGG nGGnACCGTG GCTCA	415

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

TACTTTTATT CATTGATGAA ACGAGTCATT GAGCACACGG AGCACCGGGG TGAACACGTG	60
GATGTCACTG TGAAGGTGCT GGCATTTGTC CCGGGAAAGTG CAGGTTGTG AACGGATCCT	120
GGAAGGCAAG CGCTGCAGAG GTGCTGTGCG CAGACCACGA GCGGCTCTCG CAGCCATCTG	180
TCCCAGGAGT TGAACATCTG CCGCTTTCTT CTGCGAAnTG TGGCGTTTCC AAGGGTTTTC	240
TTCAAGAGTG GATGTTGAGT TAATGATTGT TGAGATTAAT TACTTCATCA GAATTCTTTA	300
AGAAAATGAC ATTCTATTA ATGTTCCCT TCATGCCAA ACCACAACCTT TTACTCTTCT	360
TGATTTAACC TGCCTGGTGG CCTGTGAGTT AGGAGTTAGA TCCCCTCAA ATTCTGCTC	420
ACGTATTCCC GAAAGCTCAC GCTCCAGTT TTATCTCGCC GCCTCCCGCT GAGAAGGAGC	480

968

GTGATGATGC GAACTTCCGC TGAGAACTAA TTATGGAGAG GCAGTGAAAT

530

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

TGCTCGCCAC AGGGGACATC ACCTACTCCC TTGGCCTCCC ATCCAGTAAG CCTATGAAAG	60
ACCCCCAGAG GAGCTCTCGG GGATGGAGAA CACACGAAAG GCAGGATACG GAACACGAGA	120
ACAGCTTTAG GGGTATTTCC ATCAATGTCT GCCAACCGTC TCCTCACATT TTTGGAGATG	180
ATTTTGTGTTT CCCCAGGTAA AGTCTGTATT GCTGGTGAAT GCAGAGGTCC CCTGCTATGG	240
ACGGGCAGCT CCCCGCCCCC TTCCCCATCAT AACCAAGCCT ACTCCAAAGC TCTGACTGGT	300
TGATAACCCAG CTAGCCTTCC TGTGAACACT CACCAGTCCT CATAACGTGA GTAAAGGATT	360
TTCAGAGACA CTTTAAGGTA AGGCCAAATG CGATTTCTCT ATTCTACAAA AGGGAGCCCA	420
GAAGTGGTTA AAGAAGTTCA CTCAAGGTCC CTATAACCCA GCAACAGCAC GCACAGTGCT	480
TGGGCCTTAG GATCCTCAGC ACAGTTCCAG TGCTC	515

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

AGGACACTGT TCAACAAATG GTGCTGGAA AATTGGATCT CTGCATACAA AAGTATAAAA	60
CAAGGTCCCT ACCTTATACC TTATACACAA ATCAACTCAA AATGGATCAA GGGGGGCTGG	120
CGTTGTGGCA TAGCGGATAA AGCTACTGCC TGCAGTTCCA GCATTCCATA TGGGTGCCAG	180
TTCTAGTCCC AGCTCTCTGC TGTGGCCTGG GATTGTGGGG AGCAGGGTCC ATCTCCCGCA	240
ACATGGTGGA GCACCCGGGA GACAAATAAG TACTGAGGCT GTGGACTGAn TGAAAnCCTTT	300

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

TGnGAAAAGA	GAACAGAGAC	CTTAAAAGGT	GGCTTGCCCA	GAGCTGCCTG	CTTAGCCTGT	60
GGCAGTCAAG	GGTACTAAGT	AGGGCTCGTT	GCTCCCAGTC	CAGTGCTGTT	TAAAATTGCC	120
TCTTTGTGTT	TCTCTTTCTT	TTTCTTTCTT	AATGGGCAGG	CCACCTTTTC	TGGACTGCTT	180
TTAAAGAATT	GAAAGCTGAA	TATTAGCAAT	TTTCAAAGA	CACGTATAACC	TCTAGTTGCT	240
CCTCTTAAGT	GATAAGTCGT	ATCTGTTTTT	TGCTGTAAAT	AAAGTTAACG	TGTTCTACTT	300
AAGTATGTTT	ATTCAGTAAA	AATATTGTTT	GAATACACTT	TATCTTATG	TGTCTCTCTT	360
TACTCTTAAT	AATAACCATG	AGAATTGCGC	TTTCACATT	ATTCAAGCTTG	TAGTGCATGC	420
CAGGCCTTCT	GCTGAGTGCT	ATGTCTGTCT	GACTGTCACT	TGGAACACAG	TCCGTGTTCC	480
CTGTAGTCTA	GAAAGGCAAG	GGGACTTGAA	GACTGCTGGT	TGTCATAACT	GAGTGCTGAA	540
GAATCGAGAC	AGGACATTGA	TAAATGATCA	TTGAG			575

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 704 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CTATTTCTGT	TGACCAAATT	TCAGCCAAAT	TATACTCAAT	CAGCATGCTT	TCAGCAAATA	60
TCAAACCTCAA	ATTACAGGCT	GGTAAATACT	TAATACCTTG	CCTGTACATT	TAGTTGGGCT	120
AATAGATAAG	CAGAATCAAC	TTGGTAGGCA	GAGTGTGCCT	GCTCCTAACT	ACACTGTGGT	180
ATGTGAGTTG	AACGAGAGGA	ACGTGGTTA	TGTAAGCAGT	GAGAGAACAC	ACAAAGTGTG	240
AGGAAGAAGA	TTTTGGAAGA	CTACAAAGAC	CAAACCCAGG	AGAGGCCATC	TCTAGCACCC	300
AAGGAGGTCG	TGCGGAGGGT	GAGTGTGGTG	ACCATGACCC	TGCTTACCGG	CACCCAGCCC	360
TTGGCTnCCA	TCTCCTCAAC	CCCATCCCC	CTCCATTCCC	ACATAAAGGG	GGGAGAAAGT	420
CATTAGCAAA	GTATCAGAAT	GATAGCAGCA	AGTGATGAGA	ATGAAAGGAG	AAGATGTTGT	480
AAGCAAATAC	AGTGGAGCAG	TTAGCTGAGA	TTCTCTGAGC	AATGCAGACT	CAGCCTGGAA	540

970

GCCCCAGCTCC ACCACAAACC ACGGGAGGTC TCCCCAAGTC ACCTGTCTCT GAGCCTGTTT	600
CCTCATATGC GATATAAAGA CAACAGTATT AAAGCATAAA TGGTAATAGT TCTATTCCCTA	660
CCTTGAAAAA TATTCTTGTG AGCATTTGAT GTGATCATAT ACGT	704

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

GAAGGCCACAC GGGGCTCTGA CCACAAACCC AGGCTCCTGn CCCCAGGCCT GCCCAGGCC	60
CTGCTCCCT CCCCTCTGC AGCCCCCTGAC CAAGTGCCTC GGGCATGATT AGAGTGAGGG	120
AGTGAGGCCT GCAGACCTGC AGCTGTCCTG CCTTGCCCCA CGCAGCAGTT TGGAAGTTAC	180
CAAATGCCTT CCGTGACAGG CGGCCCCAG GACCGCGGGG TGCGGGGTGC CGCGGGAGTG	240
CGTGCAGAGG GCCGGCTGTG TGACCCCCAGG CAGCGGACAC CCTCTCTGGA CCTGGCCGGC	300
CCCTCGCTAA TGGGCTCTTG GTCGCTCTCC TCCCTGCAGC CTACTCTGCA ACCAACATGT	360
TCCCTGCAAA CCGTTCCCTT GGGATTAGGA CCAAGGGATC CTGTGGGCAG CTTTTAGGTA	420
CAGGTAGGGG CTGAGAAGCT GCCGGAGGGG GCTGGGAGCC TGGCAGAnGG GCCGGCCTGG	480
CCTGGGGGGC ACACGGAGAG GAGAAAGGGA nCCTGC	516

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

CCACCTCCAG CCGTGTTCAA ATTAATCTTG GCAACTACCT CATGTCTGGT TTCCGTTGGC	60
AACCAGCCAG GCTCTGGGCA TGACCCCTCTC CAGTGGACAG CCTCTGCCTC CTGGGGCCTG	120
GCCCGGGCTG CCCACGTGGC TTTTGGCATG TGACCCCTGGC CTTCCCTGGG GTGATCCCGG	180
GGCCGGCGGG CGGCTGGGGG CTGGGGTGCC CAnGTGAnCC CAGCTCAGAG GGCTAGGCAA	240
AT	242

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

AGGGTACAGn	GTCCTGAAGA	CAGAACAAATG	AAGAAAACAT	AAACCCGTGTC	CTGAAGGAGC	60
TTAACTAGAG	AATCCCCTTG	CAGGGTCAAC	GACCAATCCC	AAnnCTGTGT	GTACAATAAG	120
TGGTCCCTCA	AGATCACAGA	TCAGGGACAT	TCATCTTAGG	TTGGGTGGGT	AGGGAGAACT	180
TCCCAGGGAG	GGGACCTCTA	TGTTGACCT	GAATACTAAA	CTAGCCAAAA	AGAGCCAGCT	240
GAGAGAGGGA	GGTGGGGACA	GCTAGAAGAA	GCATTCCCAT	ATTTAGTGAC	TACCAAGTAGT	300
TCCATATGCA	CCTAGCGGAA	GTGAAAAGTT	GAGGCTGGAG	GAGTTGGGAG	AGGCAGATCT	360
GAGTGGGTGT	GGTTTGTCAG	GTTGAAGACA	GGGAAGACCA	AGGACAACCA	AGGAGTAGCA	420
GGCAAGGGAG	TGACGTGGTC	AGATTGAAAC	TTCAGAAGGT	ACATTCTGAT	TGTTTGATGT	480
TAATAGTGTA	TCAGGGGAGT	GCAAACAGCC	AGGGGGACAT	TGCAAGTGT	TGAGAAATGG	540
TGATGTCCA	GCATTCCCTGA	CCCAAGTCCT	GCCAGTGGGC	AGGCCTGGAC	ACGTnCCAGG	600
GAAGAACGGC	AAGACCGAGG	ACTGTCAGGA	TGTCAAGCGG	GnGGTAAGGG	G	651

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CTCGGGTCAC	TTTGGTTCAg	TGGTAAATAA	nCAGTGAnGG	ACGCTGCCCT	AGGAAAGTAG	60
GGCATCCGTG	GGAGCAAnGA	GGGGCTGCTT	TTGGTGCCAG	AAnCTCCCAG	CCCCTCACCG	120
GTCTCTGTGC	GGAAGCCCAG	AGTCTCCCTC	CAnCCTCCCT	GGTCTTACCT	GACCCTGACC	180
CCAACAGCAT	GGCTGCCAAG	TTCTGAAGAC	CCAGGGAAGG	TAAAGGATAT	GAAACCTCAA	240
GGGCTACTTC	TGACTCCTGG	CCGTnGGGGA	AAGGGATGGA	CTGATAATAT	CCTTAnTCTT	300
TTG						303

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TTTCCTAGAA	GTCTCTCTAG	GAATTCCTTG	GATTGGCTAG	ACTGGAGCCC	CATGCCACC	60
CCAAGGCCAA	TCGCGGACCA	AAAAAGAACAA	GAAGTACCCC	AGCTGGCTTC	ATGGACACGT	120
GATTTGACCC	CTGAGGTTGG	GTCATTGCTC	CCAGAACTCT	AACAGAGAGG	GCAGGAAACC	180
AGCTGTGTCT	GTGACAGCCA	GTCCCCCAGT	CCAGTACCAT	CTAAAGTCAG	AACACAATCT	240
GAACCATGCT	GTCAGTCAGG	CTAGGGACGT	CACCATCGCT	GGAGACAGCA	CCCCTGCTGT	300
GACCTGTGCT	GCCCAGTGTG	GTAGCCACTC	CAGTTACCTG	AAGTTAAATC	AACTCCCCGG	360
TCACACCAGC	CACACGGCAG	GTGCTCCCCA	GCCCCCACGTG	ACGGGCGGGC	TACTGCTTGG	420
GTCCAGACTT	GGAACATTCTT	CTTCAGTGCA	GAAAGTCCCA	CCAGTGAGCT	CTGCCGGCnC	480
CCAnCCCAAnG	CCCCCAGTAA	TGAGGCTCCC	GGGCAGCTGT	GAGGCGAGGG	TCTTGCTGCC	540
CATCAGCGAC	ACCAACAnCG	GCTTCCCCCA	GCGCAAACGG	GAATGGCAAG	AGGGGGAAACC	600
CCCAGnCCCG	GGGAGCCTTG	AAGGGCAA				628

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

TGAGGCCACGG	nGCCGGCTTA	AATGGAAAAT	TTTACACACA	CACACACACA	CACAAAACCT	60
AATTTCCTTGC	TTCTCTTGTC	ATATCAGGAG	ATCTGGCAGT	AGTGGGGTTG	GATTnTGGGG	120
TGGTGATGGn	TGGnTGCnGT	GGGGGTCnCC	TTGAGCCATA	ATGCCACTG	CTCTTCAGCT	180
CCCTTACCAACC	CAGGATGCCA	GGGGCCCCAG	GGCACTCTCT	GGnTTTCCCTT	GCATTGCCAn	240
AGTTGTGTTT	TTCACAGTAG	AGAGACATTT	CTCTGTGCTT	GTGCGTCTAT	CTTAGATAGG	300
GATTGAAAAC	AAATCCAGAG	GCAGCTATAT	TTTCTAGAA	AAAATGTGGT	CTGTGTTGTG	360

973

CATGCnTGCC TGGTCCCTGC GTAAACACCT GTGnTGCTTT CCAGGGTGTC TATCCCAGGC	420
TTTCCAnTCT GGCCTCTTG TCACACA	447

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAAATACCTG ACCTCTCACCC TCCCACATT TATCATTAAG AATCTGAAGT CAAGAGTGAA	60
ACTAACTTGC TCAAAGTCCA ACAGATTTTC CGTTCATTTT TAATTAAGTA TAAGTTGGT	120
TGTTGTTAAA TGGGTTCTGG TGCCATAAGC ACCTACCACA GTGATTAGAA ATGAAGGCAG	180
ATCTTGAGTC AGATTCTAAG CTCTACGGCC TCTGAGTACA GGGCTGACTG ATTCACTGGC	240
TTTTGTCCCTT GTTAGCTTGC TGAAATTGCT TGCTTAGCAG TGGACTGGTA GGCATTGTAG	300
CTGGAACGCA AGGACAGAGC CTATAACTCT TCTACCAACT CATGTCAACC TTGTGCAAGT	360
ACTGAGACAG CAGCTGGGAG AACAAAAAGA TACAGAGATA AAAGAGGGAT AGATAGCTGT	420
ACCTTCATCA TGGGAGTACA ATGACGGATA AGGGGAAATC CATTCTAAAA TTTAGGCCA	480
GGCAA	485

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

ATCCTGTTAC CGTGGTATCA GCTCCCTATA CTGTCTTTAC TAAACACAAA AAGCGTCTCT	60
CTGCGGCACT GGTGTCAAAG CCAGTGAAT CCATGCTTGG GCAGTGCCGT GTCCCTCTCAT	120
CTCCCAGTTG ATTAAAGTCT GTCTCAGCG GGATCATGTG GAAGGCTGGG ATCATGTGAT	180
GAGTTGACAC ATAATGTGCC TTTGCCGAGG CAGTGGGGAG GGGAACAGGT CCAAGAAGTT	240
ACAAACTAGC TCAGAGTGTGTT CTCCGCAGAC ATCTTAGAGC TTATTGGAAC ACACACACAC	300
ACACACACAC ATTCTGATTA ACAAGCAGTT TTAAGACTTC AAGAGGTGCC AAAACCCGGC	360

974

ACTACTTGAT ATTGTTGTTA TTTATTGGGn AGACATTAAC ATCCACGGnA GACAACCATA	420
GTTCA GTGTC CCTGACCCAC TAAGCTGCTG CACTTTCCCT CATTGCTTTC CAGCCCTTGT	480
TCAG	484

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

AGCCTGCACC AGGGCTGTGC TGGACTGTGG CGGGGTATGC AGGGGAGCGA TGGGATGTCC	60
ATGGACCCGT CGGCCCTCCC TGTCTGTATT AAGTCAGCGT CATGTTGCTT GAACTAAAAT	120
AGCTGTGAGA AGCCACTGAG GAAGAAGGTT TACTCGGCTC ATGCTTTGG AGGTTCACAG	180
TCTGTGATTG GGAGGCCCCA TTGGTCCGGT GTCTGATACG GGCATTGGAT GGTGAAACAC	240
AGGGCAGAGA GAACCACACT GGGAACGAGG AGGCAGTGAG AGGCAGGGAG CCTGCTCGTC	300
ATCTTCTTCC ATGTGGCTCT CCCTGGAGAG CACCAAGGATT CCATCACAGG ACTCTACCCCT	360
ATGGTCTGAT CCAATCTAGT CACTTTCCAA GGCCTCCCCCT ATACGCATCG CAAAGGGTTA	420
ATTCCAGCCT TGACCCCTGAn TCTGGTGAGC AGGTCTCCAG CACACAAGCC TTGGGGGCCA	480
ACTGGACTAT TATCCAATCC GTAGTACTGT CCCCCAGACAn AGCTGGCGT GCTCTGnCTT	540
CTGGCGGTGAC A	551

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

TGCCCTCAGG GCCCACGGTC AGGCACAGCT CCTCCATGAA GCCCTCCTTA GCCACTCAGC	60
CGTCCCTGCT GTCACTGCAC TCCATTCTC CAACAGACCT CACCCCTCCC TAATGTCTCC	120
CTGGCTTTGA ACTCCAGGTG CCCTCCTTGG TTCTCCTGGA CTCCAGTCTC TGGGTTGACC	180
TCAGCTCTGC CAACCACATG GGCTCACAGG GACCCGTTCT CTGTAGGTCC CACCCCTCAGC	240

975

TTCCAGAAGC CTCTGGGTTT ATAGGCTGAG AGTAAAGACA AACTCAGAGC ATGCAGGAGG	300
GCAGACTGAC AGTATCCTGC TACGAACCCA GCAGTGTAGC CCCGAGAACCA CCTCAGGTGA	360
AGGCCAGAAA GTCTCCTAGT GCAGTAGCCC CTGCACCTCA GACCTTCCTT CTCAAGTGAC	420
AGTCTCTCTC CAGTGTCTCT CAGCTCAGCT GCTCTTGGCA AAAGCTTCCT GAGCCAGCTG	480
GAGCACTGAC AGTACCAAGC TGTTCCAAG AGCATGAGGG GGTGTCGGCA G	531

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAGAACTTGG CTTTGTAGGA CTGATAGTCT AACTATGTC TCTAAGAACT AGAAAATGCT	60
TATATCGCCA GTACTCGAAA ACGTGTATGT GTTGTATGTA TGTGTGTGTG TGC GTGCAGA	120
TTTGGATT TATTAAATA TAAAATGCAA ATTATTTAC TCTAAGTTGA ATCTCACTGA	180
AATGAAAATG AAAAGGCAAT ACTATTCTT TAATATGGTT CACTAACCTT GTTCACACCG	240
TTACTGATGC TCGGTAnGGG TTTGCCGACC CCAGTTCTTC TCAACCC TTG ATGATTATGG	300
AGGATTAATT ATAATTGAAA ATGTGAAAAA AAGAGACTAG ATCTAATCCA AAAATCAATT	360
TGGCATAGAA TTTAATAAGA GATAAAAGCT CAAAATTCTA TAACTAACAA ATGAAAAATA	420
TCAACACGGG AAAAAGGAGT TTAGTTCCCA GCATCCAGGC CCGTACCGTG TGGATGCCTC	480
CTGGCCTCTG CTCTTCATCA GCTGCGTGAC AAAGGCACGG nCTCAC	526

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

AGAAGATATA TGAAAAGCC TCTTGATTTT TAAAATTTAT TTATTTATTT ATTTGAGAGT	60
GACAGAGAAA GATAGATCTT CTATGCATTG GTTTAATTCT CAAGTGGCCA TAACAGTCAG	120
GTCCTGGCCA GTTCAAAGAC AAAACCAGGA ACTTAATCCT TCCCTTGAGA GGAATACAAG	180

976

GATCCAACTA CATTGCCAT TGTCACTGC TTTCCCATGT GCACAAATCAA GAAGCTAGGT	240
TGGAAGCAGA GTATGTAGAA ATCTAACTGG CACTCTGCTA ACGGTATTCC AGAGTCACAA	300
TTAGTGTGTTT AAAACTACTGT GCCACAATGT CAGCTCCAGC CCCTTAATT TGATAGAAAT	360
GTGATAGTTT TAGAATTATC AAATTACAG ACTATGCGTA TGTACAAAAT TGCTAAATAT	420
TAAAATATCC ATTTTATGAA GAGGTCCAAA TTTGATAAGA GTAAATAAAG GAAATATATA	480
TAAAATGCAT ATAGTGAAAG GAAAAATT	508

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGAACAAATT AAGTTCTTTC TTATTATCTT TCAACATTTT AGTTTACCT CAAAATGGC	60
TTACTTCTAC TGAAAACAAT TTTCTTTATT TCTCAGAATT AGGTTTTGT AGACACACAT	120
CTTATTTTTT ATTGAGTTAC TAAACACTTG AGCTCCTATC TATTCAATGG TAACCCACTA	180
GAAGGACAAA ATGTATAAGA CTAATAATAA ACTTGCTGG AAGATTAGAA AAATTTATTA	240
ACTATTTTn CTTTTGTTGT TTAATGCCCT AGTGAATAA TTTCATGTTT CTAATATACT	300
ATAGTGTGTG GGTnTGTGTT ATTATATGGC ATACCAATAC AATTCTCAA AAGGCTATCA	360
CAGCCATGCT GATCATTTC TTTGGATGAA TGGGTAATT TCAGTGGAGG TAATGCAAG	420
GTTTCCCATA ATTCAATCATC ACAAAATCAC ATCTTACAA TCAGAAT	467

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

TGAAAACATAC ACTGTATTTG AGGAATGnAA AATAATCTTG GAGCTCCCTA TCTTGCCTTA	60
TGTAAGATAA GCACTCTGTG TGACATTGTC AGTTTTAAA GAGCATATCA TATAGAATCG	120
ATTGGTTCTC TCAGTAGAAC TGCCAACTAT GGTATTTATT TCATGCCTTC ACATCACTCT	180

977

TAGCAGGTCA AAAATCATTG TCTTGTGAAC ATCTAAATTG CTTCTTTAT ATATTTATAT	240
TAGCAATACC ACTGAAGGGC AACCCCTTAGA TTCCGTGGAC ATATGGGTTG TTTGGCATCG	300
GCATCTGTCA GTTCATTAAT CACTAAAGAA AATTTGGCTG AATTAATTTG TTTCCGGnTA	360
TCCCTTTATA GTCGTGCGTA TTAAGTCCTT ACCAGATACC ATCTTAGGCA ACCCAAGACA	420
CCTTCCAAGA TAAGAGTTTC ACCATAGTTA GCAAAGTCAG AGCnAAAnGT AACATC	476

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

TTTTTCAGAC AGAGAACACG TAACGTTATG TGGAAGACGG GGTGACAGCA GGGATAAAGA	60
GATACTCCAT GCTCTGGTGC TGTGGCACGC CGAGTGAAGC TGTTGCCCTCT GATACAGGTC	120
CAGTCGCAGC TGCTCCGTGG CTTCGGACCG GCAGCGCCCC GGCTGGGGAG TGAACCAGCC	180
AATGGAAGCT CTCATTCTGT CCCTTTCGAT CTCCCCTCTG TCACCGTGTC TTTCAAATAA	240
GTGAAATAAA CCTTTCAAAA AGAAATTTA TAGAAACACG ATGAGATTCT TTTTAAAAAC	300
AGTTGTAGAA AAACTTGAA AACTTGTAAAT GCTAACCAAG ATGGAGAAGA CAAGATAGAA	360
AAAAGGAAAA GAATAAAAAG GTATTAGAA GAGAGTGAAA AGCATGGACA AAGATTGTTT	420
TTTCTTTGT TTTTCTTCTC AAAGTAGTGG AGGGAAAAGA GAGAAATGGT GAGATGTAAAT	480
AATGAGTACG AATACGGTTT GTCCTGTCTT ACTCT	515

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GGATCCATCT TGCTACTGAT GGTAGCAACA GTACTTGCCA ATCAGTATGC ATTGAGTGCT	60
TACTGTATCT GTGCCAGTCG CCAGGCTCAG CGCTTGAGAG ACACAGCCTC CCATTAATG	120
GTAACGGACT GGCAGGACAC CTGCTCTAA ACCTAGAAAG AGATTACCA AACTTCTGTG	180

978

TTCAGGAGCC CAGCAGAGAG	TTCAGGTCA GAGGAGCCTG CCCACTCCCC ACGTCCAGTT	240
CTTTTAAGGG TCTCTATCTT ACTAGGGCAG ATAAGGAGGA AATGAAGGCA GGTGAATAGT		300
CCCTGCACCC CAAGTGGACA CTTTGCATCT CTAAGCAACT CACCTGTGTG CAGAAGCTTG		360
TGGCATTCCA GAAAGAATCC ACTTTGAGCT CACCTCTCAA GGGGACACAG AnGCAGTGCC		420
TCCAGGTCAA GCAGTGGAGG AAAGGGTGTG GGTCTTGGAG CAAGAGAAAA CTCAGGGGAC		480
TATGGCCAAA CGGGGGACAC TGTCCTTC		508

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

AGCATAATCA AGCGGATTAA TAACAACCCA TGGCCAATGT CCTATTGAAT GGGGAAAAGT	60
TGGAAACATT CCCACTGAGA TACGGTACCA GGCAAGGATG CCCACTCTCA CCAC TGCTAT	120
TCAATATAGT CCTGGAAAGTT TTAGCCAGAG CCATTAGACA AGAGAAAGAA ATTACAAGGG	180
ATTCAAACGT GGAAAGAGGA AGTCAAACCA TCCCTAGTTG CAGATAATAT GATTCTATGT	240
ATATGGGATA CAGAAGATCC ACCAAGAGAC TACTGGAACT CATAGAAGAG TTTGGTAAAG	300
TAGCAAGATA TAAAACCAAC ACACAAAAAT CAACAGCTTT GTATACACAA ATAACGCCAC	360
AGCTGAAAAA GAACTTCAAA GATAAAATCCC ATTCAACAAA GCCACAAAAA AACATCAAAT	420
GCCTGGGATA AATTAAACCA GGGTGTCAA GATCTCTATG ATGAGAnTAC AAAACCTTAA	480
AGGAAAGGAA ACCGGAGGTT ACCAAAGGAT GGGAAAATCT TCCCnGTTCC TG	532

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

CCTTCGTTCA AGCAAAATAT TTCCCGTGGG AATAACTTCA ACACCTTGGG ACTGCGTCAT	60
CCTTCCCTAA CTTCATGAGG GAACCTTGGC CAAACTGCTT TTCGATCTGG AGGCGCGCCG	120

979

CCTCCAAACG CCTTCATCTT TTCTTCAAAA GAAGAACTAA CGGGAACATC CCCTTAAGG	180
CTTTGACAC CACAAGCCTC CCATGAAAAA CCCCGCGCAA GGnGCAAGAG ACGCGCTAnC	240
A	241

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

CTTCTGATTC TATCTCTGTA TTGGTTATTG GTCTGTTAG GTTTCTATG TCCTCATGGC	60
TCAATTAGG TAGATTGTAT GTGTCAGGA ATCTATCCAC TTCTTCTAGA TTTCCAAGC	120
ATATATCTGT AGTTTGTGAT TATTCTTTT ATTCTGAGT TATCTGTTT TGCACTCTCAT	180
TTTTAATCTC TGATTTATT GACTTGAATG TTCTCCTTTT TTTTTTTGTT AGTTGGGCCA	240
ATGGTTTATC AATTTTGTG TTGTTGTTT TCAAAAAAAA GCTCTTGATT TCCCTGATCT	300
TTTGTATTGT TTTTGTGTTG TTTCAATT TTTTATT TCTCTAGTTT TAATTTCTC	360
TAATTTTGGT TTTGTTTCT CTCTGTTCT CTAGGTCTT TAG	403

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

TGGCTCTTTC TACAGATAAA TGTATATTCC AGAGAGCATT TTTCATTAT CCTTACCTAC	60
TGACAATCCT TATACTCTGG TATATGCAGT GAATGTGCAA GTCTCCTCAG AGGAAACAGT	120
CAAGAATGAT AGGAGCATCA GTTACAGAAAT TTTCTGCTGA CATATGTGAT ACGATTGGGA	180
GAGTACCTTT TCTCTACCTT CTAAAACAAA GAGTTAATCA TAGCCATTAA TTTTGAGCC	240
AGTGCAACCA AATCACGAGC AGCTCCAGAG TCAGTTTAA GATCAACTCC AGAGGAAGAA	300
ATCCCGTAAC AGTCTCCCTT CTCCATCCTT CCTCCCCCAT AACTGGTGCT TGCAGTGCAG	360
TCAGAACTTC TACAGATCAC AGACATTGTT TGCCCAAGCT GACCAATCTC TAAGGCGGGT	420

980

TTTTCTTCCC CCCTTCAAGG ATACTTCATG TTAACAGCTT GAGGGCGTTC AATCAGCACT	480
GCTTTGATCT CGGGCTGGAA CTATAATTAT TTAACATTGT TACAGGATTT CTATAATCCA	540
CCCCACCATT AAATCCCTTT TACACCCCTCA TCTTCTGAGG CCTAAATCTG GCATCCGTAn	600
ACTTGGTTTG TCT	613

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

AAAAGAAAAC TTCTTAGAAC TCCACATTCC TCAATTATCA CCAACTTTTC TATTGCTTTT	60
CTTAGAAAAA ATGTTTTAAC TTCTCTGAAC TTATCCATAT CACTCAAAAT TCTATAGCAA	120
CCACCTATTG AAATGGTTCC TTAACAAATT CAATTATCAG CCACCTGTAA ATCATTCAAG	180
GTCATTGATA TAGTGAAATA TTTCTTGCT ATGACCCAGG GAAGATACAA TCCTGTTTT	240
ATTTCCAGAA AAAGTTATCA CTGCTAACAT TTTTGCAAAA GAAAGAAAAT GAAGGATTAA	300
GTTTACTTTT TTTATCCTGA TCACATAAAC AATTTTCATC ATTCAATTGT AGCAGACTCC	360
TGCATTAAAA TCAATTAAC T GAGTATTCA TTTAAAACA ATGGAGAAAA GCAATTAGCC	420
TACTAATATA GACTGCATCT GTTGGTGAAC TAAAGGTAGA TATTTTGCAC CTCTGGACAC	480
ATTTTGAGG TACGCTTGAT AGGATTTGTT TACAGACAAG AGAGGAGTTG TGAAAG	536

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

GGGGTAAGAG nGCCGCCGGT TTTTGCCTTG AAnTTTGAAT TGAATTTTA AACCTTGAAG	60
AATTGGGGGG GATTGCAATT GCCCCCTGCG GTTGAATT TTGCCAGGT ACAAGCCGGG	120
GGGGTTATTC TTCTTCAAAG AAAGAnCGGT GGGTTTGTnC ATGGAAAAAA GT	172

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

CCGGCACCGC AAGGnAAGGA TTAACCTACT GAGCTGTGGC GCCGGCCGAT TTATTTATTT	60
GAAAGACAGA GTGACAGACA AAGAGATCTT CCATCTGCTG GTTCAAGTCT CCAAACATCT	120
GCAACAACTG GGGCTGGTCC AGGCTGAAAC CAGGAATTCC ATCCGGGTCT CCCATGGGTG	180
GCAGGCACCC AACTACTCGG GCCATGACCC ACTGCCTCT CAAGTGCATT AGTAAGAAC	240
AGGATCCAGG CCTTGAACCA GCACTCTGAT GTGGAATGCA GGTGACACAA CCCCTGCC	300
CCAACAGATT TATTCTAAGA GGTTTCATTC TATACATTCT GACAAAAAGG GGAAAAAAGG	360
TGCCATTATA GACTTTTTTA TAAGAAAGAT AGAGGTCTTG GTATGAAAC TGTAATCTCA	420
AAAGAAAAAT AAAAAGCCTA AGGTTTCAA AATAGTCCTT AAAAGTAATA TCATGACTTA	480
GCTCTTTTT ACTGATTGT ATTTGGAGC GTTTCTAAA TAGTTGCAAT TAAAGTTATA	540
TTTATGTATT TnAnATAAAAT ACAAAATGTAT ATAGTACATA TACTATACCT TTATACTTAA	600
AATATATATT CATTAAAGAA TGTGACACCA AGGGCAGGGC ACGG	644

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GTGCACCTCA CAGGGGACCC ATGCATGCTC TGCCTGCGGT TCCTGAGCCT GTCTTTCTC	60
TAAAGCACTG GCAGTCTCTG CCTCCCTGTC CTCTGCCAGC CCCACCTCTC CTGTCCTCCT	120
CACCTCCACC TCTCCTTTT CTCCTGCCCC TTCATGCCAT CACCATATTT TCCCTGCTGG	180
AAGCCCTCT CCCTGCTGTG TCTTACAGC TGTCTCCTCC AGCCCTCTTC CGCACAGGAA	240
CCAGGCTGAG TCCCTGCCCA GAGAACCTGG TGTCAATTCCC CCAGCTTAGC CAACGCAGTG	300
CACCAAGAG GCAGAGAACCA GGGGTTGACC CTTCCCTCCCT CTGCCTCCCT TTTGTCTCCC	360
CACTACCAGC AGCTTCCCCA GAATATACCC ACCTCCAGTC AGCACTGGGG GAATCTCCGCC	420

AGGCCAACTC CA

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

TGTGTGTTAT TAAAGCAGGT TACTGATGCC TTGGGTTGG TTTGTGTCTA ACCACAGGTG	60
GGTTTGGCTC TTTCCCTCTT CTCCCGTGTGTT CCCCATAGCA CATTGTGGTT TCTGGTGTGG	120
ACTCTGCACA GTACAGGAGT CTGGGGAGGG CAGCGAGTCC TGGGAGACCC TCACAAAGGG	180
CAGGTCCAGG TTCAGATGCT GGCTCAGCTC CAAGGCCTGT GTGGTCTTGG GAAAAGCCCT	240
TTAGCCACCT AGTTCTTCTT TCCATGCCCTT CAGTGAGCAC GGCATCCACC TGCGCTTCT	300
GGTAGTGCCT CAGTGTGGTG ACACATGGAG CACATGTCAC AATGCTGACA GGGGGAGAGA	360
CGATTAGGGT TAGAGCCAGG GCAGGCCTTG GGTTCTGGGA AGACTAGCAG TGTCTAGGGA	420
TTTGTGTGCT GTGGCCTGAG GCAGTCGCTG AAGGAAAGTT CTGGAGGAGG GGTTTTGGGT	480
GTGGTCTGTA TATTGGAGTT CGTTTTGGT GGGAGAGACT GAAGTTGAAG GTGGTTCAATT	540
TTCTCCTTAG ATGTCTTCAG GCAAGTTCTC TGGCATATTT ATTTTGTGG GAAATGGCCA	600
AGAAGTTGAA AGAAGAGGCA GTnnnCTGTTT	630

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

TCCTTTGATT TGACAACCTTA TGATAGTATT CTTATACTAG TGTTGAGCTA ATTGAGAAGT	60
ATGGAGCATA CAAACACACTC CCTCTTATCC CTTGTTCTAT AGGGAAAAAG AGGACATATC	120
CTTGATTTT CAGGGGCTTT ATGGGAAGTC TCAGAGTTAG TTTTAGAGGA TATAAAAGTA	180
TCCTAAAAAT CATACTTTA AAATTGTGG TTCTGATCTT GAGAAGGTA AATCAAAGGT	240
TGTTATATTT CTTACCTGAC TAAGACAGGA TCACTGGATT CCTGATATAT AAGACGTGGC	300

983

TATTTATTCA GCAAAAGATT CTACACAGTA TTTTAAAATG AATGTTACAG AGAGTAATAT	360
GACTGTAAGG AGACTCGGGT GGGATATGGG ACCATGAGCT GGCCTAGATT CCTGGTTCCC	420
TTGAAGGATT CCATTTCCCTC AGTTGTCCAG TAGCCAGnCC TTTAAnCCTG GTGGGCT	477

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

CAAGAACATCTG CCTCTGCCAA TGTCTTGCAG CATTACCCCT ATGTTTCCT GTAGTAATTT	60
GATGATTTCAT AGTCTTAGGG TTAGTTCCCTT CATCTATTGT AAGTTGATTT TTGTATAGAG	120
CATAAGGTAG GAATCTTTTC TCACACTTCT GCATATGGAG ATCCAATTT CCCAACATCA	180
TTTGTGAAAG AGACTGTCCCT TTCAGAAGGG AAGTGCATTT AATACACTTT AGCTACTGAA	240
CACCGTAGTT AGTAACATGG TGCACGTGAG AGTACTGGTT GTTGCCCCAT GTAAGTGTGC	300
TGTGGTTCAC TGCCCCCTGCC AAGAACACCAGAGGTGTTA ATACCTCATA TCACTAACCT	360
GGGAAAAGAT CAACATTCAA AATATGAAGT GTTGTGTTCTA CTGAACACAT AACACTTTCA	420
TACCATGGnA AATTGAAAAA ATGTTAAGTA TAACCATTTT AAGTCAGTGA CCATCTGTCC	480
TGGAAACCCn ATAAAGATAT AGTAAGTG	508

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

ATGAGAAAAG ATTGGCAATC GTTGAGGAC CTCCTGATAA CAGCGATAAA AATCGTCATG	60
CTTATTACAA TTCCTGCGAC ATTTTTCGTG TTATTTTCAA GTGACCGTAT CATAACGCTC	120
GTGTATAAAA ATGCTATTTT TAACGAACTA TCCGTGCGCA TGACCGCTAC CATATTCGA	180
TGGCATAGCG TGGGAATGCT TGCTATTGCG CTGAATCGCG TTCTCATCTC CGCCTTTAC	240
GCGCAAnACAA CTCTTTGCC CCTATGATTG CAGGAACATAT TTCATTGAG ACAAAATATCA	300

984

TTTAGCAAC ACTGCTCTTT ATTCCCTTAG GAGGTAAAGGG CATTGCATTT TCTCTGAGCG	360
CGCGAGTAT GGTACAGACC GTTTTTTAT GGATGTTTT AAAACGATCG TGCCAGATAA	420
CTATCCCTTC ACTGTATAAA ACTTCCCTTT ACTATGGAGT GAAAATAACT TTATTTCTG	480
TAATCGCGCT GGTACCCACA TGGGCAAGTT CTTTTTTAC GGCGnATT	530

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTACCTCTGC TTCTCAACAA CCCGACCTTG AGAAATCATG AACAGCCAGG GGACAGGCTG	60
TGCAAGGTGC TGGTCAGATT GGGAAAAGGC ACGGGCAGTG CACCTGGCGC ACGTACATTC	120
TGCACCCAC CCTTCACTCA TCCTCGGCTT CAGCCTTCCC TGTGCGGAAT CAGGGGCCA	180
TTCTTGAAAG GGGGGAAATC ACAGGAGCAC AGTTCATGCA GTGCAAGCTG ACCAGGGAAA	240
CGTGCAGGAGG GGGATTGAG CTCGGCCAG CGGGTGCTGA CGTCAGAACG AGGGTGGCG	300
CAAGAGAGGA TGATTCTGGC ACATAGAGGT GAGAGGGCCA GGGCTCCAGG CAGCTCTCCT	360
GGCCACTCCC CGCACGGCAG GTGGGGCCT TCCGTCCCTGC AGATCCAAGC CTGCACATAG	420
CACCCCTCTT TTAGCATTG CCCCCACGAG GCTGACGATT CCTGTTGGCT TCTGACTAA	479

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

CCATTCCAG GGCCCTCAGC CTGCCCTAGG CCCACAGGCC TGCCACGGAG GCTGTGGCCC	60
ACTCCTCATG GTCTTCGGTC CCCACAGGGC TGAGCGCTGA GTCTGGCACC CGGTGGTTTC	120
TGAGTCTGCG GAGGAGTTAG TGGTGGAGGG AATTAAATGA ATGAGAAACC CGCCCAAGGGC	180
CTGGGATTGC TGCCTCCCCCT CCCCCCTACAG AAAGCCTTGC CTCTCTGGCT CTCCGGCCTC	240
TCAGCGTCTA TGATTAAGC TTAAATCCCT GGCTTAGGCC AAACGGGGTA CCTGGTAAAG	300

985

AGGAAATCCT TTGGCTCACT CTGAGTCCTG ATAGAAGGTG CACTCAGGAG GTTCCCTGA	360
AAAGCGAAAG AGCAAGCAGG GATTGCAGC GAGACAGGGG GGCAG	405

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

GGCAATGTT TTGCTTATTC TTGTCATCAG ACAAGGGCCA TTCTCTAAGG GTTTTGATAG	60
GCAATCATTA AGCATCCACT TTACAGAACT GATTTGGCTG CTTCTAACTT CTTCTTGTTC	120
CCTAACCTT GAAAACCTCT AAAGACATCT ATTTTCTTC AGTTACTAAA ATGTAGACTT	180
CATTGACCTA GTTAAATTCA GGACCTCAG TTTTTGAAA ATGGAGTAAA TGACTGTGTG	240
ATTGCTAACAA AAAGTGTCTT AAAATAAGAA TGTTATTAT TGTTAAAAAA TTTGCAGACA	300
TATAAAAATT GTACTGATTT GGGAGTACTC TGTGACATT TGATACAGCA TATACCTTGT	360
GTAATATCCA ACCAGCATAG ATATATTTAT CTCTCAAAT ATTCAACAGT TTTTATAGTG	420
GAAACATCAA AAATGATATC TTCTAGTCT TTTAATAGAG AAATACAG TACATT	476

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

AAGTGAATTG GATCTCTTTA AAGCTAGGCT AAGTTCTGC AGCAGCTATT CAAGGGGAAG	60
GCAAGACACA CTGACAATAA AGACACGTGT ATTCAATTCA TGGGGTGACC GAATGACAAC	120
AAAGCAGATG AGCCTATAAG AAAAAGCCAT TTGAATGTGA TAGTTGAAAA TCTCTTGTAT	180
TATCTTTAGG GATATCAGGT TCATCATACA TGTGATGTGT GAGTGGATAG TGTAAAAAG	240
TTATCCTTTT TAATATTGT TTCTCACACT TGGTTCTCT TATGTGTGTG TGTATGTGTA	300
TGTAAGCTAA ATTAAGCTCT TGTTCTGTTA ACAGAAAGGT GGGTAGATGT GGTTAGAATT	360
TTCTTTTCC TGTCACACTT TCTAAGGATT ATTTTAAGA AATGGTATCT ATTTATGTCA	420

986

TGACTGATAA GTATTCCTT AAGTATTCAAC TGATATTTCA AAATTTAAGA CTTATGCTTA	480
ATTAAGAAAA GGATGAGAGA TCCAATTCAA TCAACCCCAT TTCTGTCTA ATATATGAGA	540
CTTCGGTGGC TAGTGGATTC CCTCATATAA G	571

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

AGGTAACACA GTAAAGGATA AATCTATATG ACCTCTCAAT ATATGCAAGA AAAGAAATAA	60
TAAATATACT GCCCACTCAC TGTAATAATG AGTACCATTA AAAGACATCA AAACCAAAAT	120
CCCATTGTGT ATCCATAGCA CATAAACAGG AAACAAGATA TCCTCACAGA AGCCAAAGGA	180
GAAAGGAGCA GGGGAACAAT GCGAAAACAG CTAGCTACAT GCATCAGGAC TTGTGTAGGA	240
CGGAAGGTGA AAGACTACTT ACTGGTAGGA GAAATTATAG CTAATTGCA GCCATGTTTG	300
TACCCAGGAT CCACCTCCCAT CAAAGTACGT CCTGGAACAG GGCTTGTAA AAGAAGCTGG	360
ACGAAGGTTT CCGTCCAAAC ATCATTACTG ATTCCCTCTC TGGCATCGGG AAGTCAGTTT	420
GGGCTTTCA AAAATATAAA AAGAAAAGAA TTACTGGAGT TTTTTCATTT ATCCAAGTTT	480
TCTTTCCAGA AAAAGAGAAT TTATTTGTA TAGTCGGTCC TTGCAGGAAC ATTTATTATA	540
ACAAAATGAC ATAGTAGAAA AGCAACATAT AATAAAATTA TATTGTCTAT TTTTTGTnAA	600
TCCCTGTAAC ACATGGCACC ACAAAACAATT CTGA	634

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

TTAGTATCTG TGGTCGTGTC ACCTTACTGT GTGAATGACA AAGGAGTAGA TGTGGAGAGT	60
GGATTAGGGT GAGAAGGTGT AATTGCAGGT GAAGGTGAGA CAGGCTGGAA GGAGTCACAA	120
AATTGAGCAC TCTTGACCTG ATATGTATTC CTCTCCCACC CTAACATATG TCTGTCTCTG	180

987

ACAGAGCACA GCCTGCTCCA CTTAGCTCCA AACCAATCAG GAGCAAGGAG TGTACACACT	240
CTGACGACAA AAGACCCAC CTACTGCCTG TGCACTTGTG CCAAGCAGCC TAATGCAACT	300
GAATTGTGAC CTTCTTGTTG TGGCAGTAGT GAGCCACACT GTGATTGTA GTGTGTCTTA	360
ATGTAAAACA ACAACAGAAC ACACAGGTAC TCTGTGCTGA AGAGGGCAAG CCAGAACACT	420
GAGCTGGGAG CAGACTAAAG TGCTGTATCC CAAGGGTGTG CTGCTA	466

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

AGAGACCAAG GGAATTATTT CAGCAGTGTG GCTCCATGGA TCAACCAAGA GACAGAGACA	60
GAAAGTGGAA ATCACCATTT GCAATGAGGC AGACACAGCA GAGACAGAAA GGAAGGATGG	120
GTGTGAAAAT GTGTAGGAGG CAAAGTGAGC AGGACTTGGT GGTTGGCTGG AGCGTGGAGG	180
TGAGAGACAG AAGAAAAAGA AAGAACTCAG GTTCCTGAGC TGTGCAATAG GATAACATGGG	240
GCTGCACITC CCTGAGCCGG GGCCTGTGTG AAAGGGGTGG AGATGAGGGT GGGAGAGAGT	300
GGAGAGAAGA TATAGTGATG AGTATTGACC TGGCACACCG TTTCTTCAGG ACACACACAG	360
GGAGAACATA GCCATTTCTG TACCTTnCG CAAGCCAACA AGAGGAAATC ATAATTGAAT	420
TTCCATGAAT ATTTAAAATC GAAAGGAAAA GTCTGAACTA GAACTATCAT TTACAGTGAC	480
TATATGTCAA GATTCTTGCC AGCCTTGTGTTA ATTTTACATA TGCACATTTT TACCTACAAA	540
TTATATCTAC TCTATCATTT TTCCTCAAGA ATCnATTGnT ATTTTTAAA GATTTTATTT	600
AnTTATTGAA AGAGATAChC nGAGAGAGAA A	631

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

CAGAAAGATTT TAGCTTCccc TGGACTTTAA AGTAAAATTG GGCAGAAAAA TGCATTGAAG	60
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988

CAGGATTTTT TTAATATCTT CCCGTTAAT GTTCTCTAGT CAAACCACCA	AAAAGAACGGT	120
GAGCAGTAGA CAATTGTCCA CATCTCCCCT TGTGTGGTCC CTTCGTTGTC	CTTGATGAGT	180
GCCTACAGAG AAACCGTAAG ATTCAAAAGC TGAGCAGAAA TACTCTGATA	CAGAGAGGGG	240
TCGTAAGTTT CCCTTCATTG CTTCATTGTG GTTTCTACAT CAGACTGCAG	CATATCGTTT	300
TTAGAAGTTC TGTGGTTGC TCTGGTAGGA CTACTCCCC CGTCCTGTTA	CTCGAGAACG	360
TTTATCCAGC GATGAGTACT TCGGTGTTAG GGATACTCAA CACAGGCC	GGGAAGCAAC	420
GGGATGATAT TTTTGGCTGG CACGTATCAT TTTGTGTACT TATTTCTTA	TCTATTCTATA	480
TTTGACGAGC CAAAAGGGT GAGGTAGGAT ATCCTATCTG CTGGTTCACT	CCTCAAATGC	540
CTCCCAACAG CCAGTGCTGG GCCAGGCTTA AGTCAAGAGA TTGATCCTCA	ATCCGAGTCT	600
CCAAAGTGGG TGACAGGGAC CCAAACACTT GAGACAT		637

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

AGTTCTAAA TGAAAATCCT TCTAAACTAA GGTCATTGCC	TTTTAAATG GAGGCCAACC	60
AATATCACGA TTAGTGCCTC TCTTCTGCTT CTGTCTCTCA	TTTCTCTTCT TCCTTTCACT	120
TAATGCCTAC ATCATGCTCA CACACAGACC TCTTCTCTCC	ATTTGTTGT CACAGAAGAG	180
ATATCAGTCA GGGTACACCT GCAAAAGCAG AAGGTGGGTG	CTTGTCCTCC ACCCATCCTG	240
CAGTTTGTAC CTGAAGATTG AAGACATATT TTGCGAATGT	TTACCAATGT CTGACACATA	300
TTTATACAGT TAGCAAATAG TAATCTGAAC CATGAAAACA	TTCCCTAGAAT ATTTACACAA	360
AGTGAACCT AAATAGAATT CTCGGTCTCC ACCTGAATTT	CATACATCTG GATTTCTCT	420
ATGGTTTCCG AGAGAACTCC ATATCTTCC TGGGGTGAGT	TCATT	465

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

CAnTACTGTT TGCATAATTAA GAAAATATAG CGTTTCCATG TATGTAGCTT TGACATTATA	60
AACTCTTTAA GATTACCACA GTGGATGTCT GATTTCTCCA CAATGTGTAACCGGGCTTGG	120
AAGTTGGCAG ACTCAGTCTC ACAACATGAA AAATATCTGA ACAAAATGAA AATCAATGAC	180
TTTTGTTTGA TCCCTCAGAG AATTGTGGTC ATGAGATAAA CCACTACCCCT GAAATCTAAA	240
AGCAGTAGAC AAATGGAATC ACAGGTGAGA TCAACTCAAT AGGGGTAAGC AGACAGAACT	300
GATAACTGCT AGGAAAATCT AACCGTAAA TTGAAAAAT CTTAGAGACC GAACTGGACA	360
GTTAAAAGAT CCTGGAAAAC CCAATTTAG TTGGACCACC AAACCCCTAT CTTGTGGTTG	420
GCACAATGAG GGCAGAnGGG TGACCCCTCCA AGGATCTCCT CCAGGTTCTC ACTCTAACCA	480
TCTGGATAAA ACTTCCCTCA GGTGTAGACA GGGTGGGGAG GAAATGAAAC ATTTGAGATG	540
CGCCCAGAGT ACTGGCCACn ACAAAGACCT AATTCCCTAA GGGGAATCAC TCAGAGCACT	600
AATCTGGCnT GCAGAAAGTT GGGGG	625

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

nTATCGTAGG CAAGATAGAC ATCCGTAGGA AACACCGTGA GTGACAGTTG CCTGTAAGnA	60
CATGGGACAT GTAACCTAGC CTAGCGGTTTC ATGATAGAAA GTGCACAATA AAACCTCCAG	120
GATCACATCG GCCTCCACGC AGCGCCTCTG TCTCCCCCGC CCCGGCnCTG GCCGCGAGCG	180
GCTTCCCAGG CTGGAGCTCG GCCAGGCCCG CGGGCGGCTG CTAGGGTCTA AGCnGACCCG	240
GGAGATGGAn CGCAGACACA GCCCCTGCCG CCTGGGGACC CG	282

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

990

GGTCAGGCA ACTCAGGCCT GTGTTGCCT GCACCTGGC CTGCAGCTGT CCCCTCCAGGC	60
TCTCCAGCTC CTTCTGCAGC TGCTCAGCCT GCGCCTTCAG CTGCTGCTCC GCCGCCGCCG	120
GCCCCTCAGG GGAGGCTGGG GACTCTGGGG TGGGAGGCTC AGCTGAGAAA GGAAGCAGCC	180
ATCAGGGGCC CTGGCCTCTG GGTTTCAAA AAGCTCCTGT CTTGGTCCTT AGCTCCTCAG	240
GCCAACCTCT TGCCCCCACC CCGGTGCTGG CCTCTTGGCT AACAACTTTA CATATTCAAGA	300
TGGTCATTAC CCTTCCAAGC CAGGACACAG AGTGCTTGAC CGTGGCATAG TGGACAGTGG	360
GTGCGCCACC CCTATTTACA GATGAGGTCT CCTATGCTCA AAGAGATAAC AAGACTCGCC	420
ATCCACCGGC ACAGACCTGC TTCCCTCTGC CACAACACCC CTCAACGGGG CAACCAACAA	480
CCATCCTGCT CCCAGGCCAA CTCTGCCCTG CTCAACCATC TGGCTCTTGA G	531

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

CCACCGTGT ACCTGGAGTT GTAGCGCCCC CTGGTGCCTAG TCTAACTAGC ATGGCACCAA	60
CTCAGGTTTG CCTCCGTCCT TGTGCCTGCT ACCCCTGTAT GCTTGCACCA TCTCCCTTCC	120
CAGAGGACTG CGCCTGCTGT GCCTTCTCTT CTCCCTTCTT CCGGCAGCTT GGTTCCCAAT	180
GTGAGGCACC CTTCCCGCA CTGGGGTGGG GGAGGCCAAG ATGGGGCTTT CTCTTGAGCT	240
TGTGGCAGTG GCAGGTTGCT GGAAGGAGCT GGGCTCCTGC CACCCCTGGG CCAGTACCAA	300
CAGCTGGCAG TAGCCCTGGA CTCCAGCTAT CTAACAAACA ACTCAGTAAC ACCATAGAGG	360
AATTGGTAAG AGCCCAGTGG GGTCCCTGA TTCCATGCTG CCCACCCCTGG GCTTCTGTTT	420
CCCCGTGGGC TCTGAAGAAA GGGGCTGGGG GCCCCCTGGT GCTGAGGGAG ATGGGGTGCT	480
GGGTGGGCCA GGTCTCAGTG GAGGGACCCC AGAGCATGG	519

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

AGATTTTGCGTGTCACTATGCAGGGGAGGTGTATGTGGCTATTGGC	ATCTGTAAGT	60
AGAGGCCAGGTGTCTCTAACGCATCCAATAGTCGCTAGCTAGGCTACC	CCTCCCAACC	120
CCCAGTCTACAGGCCTGGAATTGAGACCC	TTGAAAAGAC	180
CATTATAGTC	CATATTTAGG	
AATTTGGGCTGTAGCCTAAAGTAGTGGGA	AAGAACTAAA	240
GGGATTGTGTAAGGGTGC	GCG	
ATTTGATTAAATTTGTGCTTAAATTTTC	TTTCATTTA	300
TCCCTCTAATTGAAAGGCA		
GAGAGGGAGATCTGCCATCC	ACTGATCCTC	360
CCACCCCCAA	TTCTGGCAA	
CATCTGGGTTGGCCAGGC	TAAAGCCAGG	420
AGCCTGGAAC	CTAGGTCTCC	
TACTTGGGTGACAGAGACCC		
CAAGCACTTGAGCCACCGTC	TGTTGCCTCC	480
CAGGGTCTGC	ATTATTAGAG	
AAGTCCAGAT		
AGTGTGTCCC	TGGTGGTCCA	
GTGGCCAGGA	TTAGAGAAGG	
CCAGATAG		528

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

AAACTGGCTGnATTCATGTA	CTAATGnCCC	TTGAAGGAAT	CCTAAATGAC	TAAAATCACA	60
ACAAGATTTG	CTCTTTCAAG	AGATTGTCT	AATAAGnGCA	GAACTGAAGG	120
TTAACCAAGAT	AGAAATGGAA	AAGCATTAC	TTTCATAAA	TGAAAAAAAT	180
TCATAATCTT	TTATGAATGn	TGTGGATCAA	CACTGAGAAC	ATTCATAATAA	240
TGCCTCCTAT	GGAGTTATTT	TTTCAGATAA	ATCCAATCTG	TACAGAACCA	300
ACAnATGGGC	TAATACAAA	AGTATCCAAG	TTAAGAACGA	CTCTAGACTT	360
ACnTGGTGAT					370

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

992

TGCAGCGCGC GGCGCACGGG GCGATACAAA ACTCCCTCTG CGCACTGAGA ATTGCAAGTA	60
TAGCGCGCCC CCACCCCCCT GTCTACCTGA nGAnGGGGCG GGGCGTGCAG CGGTGACGCC	120
ACCCCTGCGCC CGTTGGCCCC TTCTGGAGGG TGCTAGACAC GGnnnGGGGG GGGGGTGTG	180
TAAAAAATGAn ATGGGTCGGG AGGGAACTGC ACCGTGCATT CTnTTTTGTG CGGGGCGCCG	240
GGGGCGCTGCT CCCGGGGTTT GGCGCACTGC CCGTTTTTC TGAGCAGCTA GGCAATTGCC	300
CGCAGTAAnT GGTCACGCC AGCTGCATGG GGCATTAAGT TTAAAAGAA ACCTTCGGTG	360
CAACGAACGA nTAAACGCAA CGGTTTT	387

(2) INFORMATION FOR SEQ ID NO: 463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

CACCTTCCTT CTACACCTAA CTTTTAAGGA TTATTTAAT TTTGAAGAGA TGGTGAATTT	60
ATTGAATGAT TTTTTCTGC ATCTATTGAT ATGATAACAT GGTGTTTGCC TTTCATTTTC	120
TTGACATGAT GTATTAGATT TATCAATCTC ATTAAATTTC CTTAAAATCT TCTTCTGAAT	180
TTTTTGAAA GGCAATTTC ATTTCTTTG TGATCCCTTG CAGGAGATGA TTGGGTTACT	240
TTGAAGGTAT GATGTTACCA TGCCCTTTT TTATGCTTTC TTCTTTTTT TnTTTTTTTnT	300
TTTTGTCAT GCTGCTTGC CTCTTCCGA TTTTGTCGCC TCGCTGGCTC AGGTGCTTCT	360
ATCAGTGTGTT TTAGCTTGGT AGTAAAAGAT TTCGGCGGCA AGGGTACAGA GCATCAGTAG	420
AAGTGTGTCG TGGCTGGnTC CGGTGAGTAC TTTAAAGnGG CCAG	464

(2) INFORMATION FOR SEQ ID NO: 464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

ATAGACATTG CAAAATGTCA AGGTACACAA TGGAAAATAA GCTCACATAT TTGTGCACAC	60
ACACACAGAG AGTAGGGTGG GTGGGGAGAG ATGGGATAGG TAGAGAGAGA GAGAAATATT	120

993

GATCTTCCTT CCATTGTTTC ACTCCTAAAA TGACTGCAAT AGCTGGGACC ATGCTAGGTC	180
AAAGTTGGGA AACTAAAGTT CCTTCTAGGT CTCCCCATATA GATGGAAGGG ACTTCGGTAT	240
TTGAACCATC GTCTGCTGCC TCCTAGAATG CACATTAGCA AGAAGCTAGA TTTGAAACAC	300
CATAGCTAAC AGTTGAACTA GGCAGTACAA AATGGCATGT GGGCTTCCCA GACAGTGGCT	360
TAACCCTTG TGCCACAGTG CTCACCCCAA CATCTGCCAT TGTGACGCTC AGTATCAGCT	420
TTGAACCAAG AGGAACCTCTA CTCTGTAGGG AAAGGGTTAA AAAGGAGGCT GGTGGCAATC	480
CCCAATCATG CCATAGACAC CTGAGGAATT TAC	513

(2) INFORMATION FOR SEQ ID NO: 465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

CAGnAAAAAG ACTTATAAAC TGAAAGTTTT TTATACATCT ATTGTCCAAG AACCTGCAC	60
AATCTAACTT TCCAATTATA CTCTCTACTT TCATTTTTAT CACTTATATA TAGCCTTTTC	120
AAGATTCAG AATGCTAACAA AAGAAAGTGA AATCACCCCTT GATGTCCAGA TAGTCTTAGT	180
CCTCATCAAT ATCATCATAT TCATTTTCCT AAGTTTCATT CTTTTAAACT GACACACAAC	240
AATCACACAT ATTTACAGGA TACAATGTGA TGTTCGTATG CATGTATATA TTGTACAATG	300
ATCAAATGAG GGTTATCAGC CTACCTACCA TCTGTAATAT TGATCTATCT TTGTAGTGAG	360
ATCAAAATCC TCTATACAAG CTATTTATA TATACATATC ATTAATTATA ATCACTTACG	420
TGTAAACACC AGAACATATA CCTCTT	446

(2) INFORMATION FOR SEQ ID NO: 466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

CAnAAAnTGCT ACTGAAAATT ATTTTTTACA GATAGCTCAA TCACCCATAAT TAACTCCACT	60
TTTTCCCATGT GATACACACAA CACACACACA CACATAATGT CTTGAACGTGT TTTCAATATC	120

994

ATTCTGGCAA ATCTGTCCCTC CCTGCCTCTT TCATACCTGT TATTAATTTG TTGCTTGACA	180
TATAATATCT CTGGCACTGG ATTGTCCATT GTTTCTAGC TTTCTAATTT TGAAGTGCCT	240
AAGAAGTTTT TTAGTTGTCT AACTTGGCAT TATCCTAATC TCAAGTGAAC ATAAAACCTTA	300
ACATGTAATT CTTGCCCTT TAAATATCAT CATGTGAAGT TGGAGAAAAT GTAGTAACCT	360
ACAGGGCATC AGTGTACTTT TGAGGGCTC CTTTCAATTAA CTTTCTCTAT CTTCATATCT	420
TAATTGCCCA TGGGATGGTG TCTTCATGAC TCCCT	455

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

CGAGATCATG TTTTATACTTC TCTTCATAAT GAATGTTTCC TATAACACAA ATCTATGTGT	60
GTAAGGTGTG GAGGAACAGA AAAAACACTC AAAGTAGGAAA GAGGAGATGA TGGAGAAAAGC	120
CCCACTCAGG ACTCAGAGCA TGGCTTGCTA CATCAAGGGC AGCAGTTCAC CTCCTCGGTT	180
TTGGAAACTG TTTCCAGAAA CAAATGGAGA GTGGTTTAAT CAAAGACGCA TGCATGAATG	240
AGTTTGATGA ATAAATTCAAG AACATCAATC TGATAATTCA CAGAAAGAAG TGAAC TGCCA	300
TAAATAGTCC TATGTGCAAA TCCCAATATG ATCATAAGCT TGCTGAGAGA GCCCAAAGTC	360
AGATCAGGGA AACTGCTAAG TGATTGAAAT ATTTAGTGGC ATCAGGGAAAG AGAGTTTGAT	420
CGGTTATCTC TGTACTCATA ATGATCCGGT AAGGAATAAC ACTCCTG	467

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

CAGGGCTTTA TTTATGGGAA AAAGAGAAAGT CTAGAGGCTA AGCTGGGTCC ATACCAAGCA	60
GAGAGCAGGC CAGGAGCCAC ATGGAGCAAG TGTTTGTAT GAGTAGCCAC AGGTAGCTTA	120
GCATGAGTAG CAAAGTGAAG GTACAGAGCA GGCCAATAGG CCATGTGCC AnAAGGTGTG	180

995

GGGCAAnAAG AGAnGGGnCC ACCATGTTCC AGGCCTTTA TCCACTCCA AAGAGGAGTG	240
GTTATGTAGC CTGATGGGCA GTGGGTTAC AGGTGGGTC AGGTAGGAAC ATGAGATCAC	300
ACAGGGGCAT GGTGAAGATG TGATCTTCCA GCTCACAAAC TTGATCAGTT TTATCCCATC	360
TGCCTGCCGA CATCAACCTC CCCTCAGAGA GATTCTAGCC CTTAACCTA AGGGCTGTTG	420
AAAnGGTAG AATTATCATA TACTCTATAG CTGCTTCCTG	460

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

CAGAATGTTT TATGACTAGG AACCAAAAAG AAGTCAGAAG GAGCCATATC AAGACTATAT	60
GTTGGATGCC ACATGATTTT CCATCAAAAC TCTTGCAAAA CTGTCCTTGC TTGATGGGAG	120
GAACAATAAG AAGCACAGTT GTGGAGAAGA ATCTGGAGGA GCTAGCGTTG GCTAACCTTC	180
TCAAAAACAC TTTCCCAGTA ATCAGATGGT CTCATTGTTT ATCGGTTAGA AAGTCAACAA	240
GCAAAATTCC TTAAACCAAA TATTAACGTG TGCTGTGGCA TTGACCGCTGG CCAGTCCGCC	300
TTTGCTTGA CTGGCGCACC TCTGCCTCTC GGTAGCTGTT GCTTTCATGT GCTTTGTCTT	360
CAGCATCATC CTGGAAAGC TGTGCTCATG TGTCTCACCA GTGGTTGAA GAAATGCTCC	420
AGGACTGGAT CCTGnCCTAA GTAGATTGTC TATCAAAACT GTACTCTTCT GCG	473

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

TGCATTTTA ATTCTTAGTA ATATTCAGTA TATTTACCTA TGTAATAATC TTTCATTGTA	60
GCCAGGAGAA TTTTCTTCCT GCCCACTGAA CTCTGATGAA GATGTGAATA ACTGGTTGCA	120
TTTTTATGAG ATGAAGGCTC CTTTGGTCTG TCTACCAGTT TTTGTCTCCA GAGATCCAGT	180
AAGTTTGTGT CTCTTATATT GCCGCAAATA CATTAATAAT GCTTCATTTC TAGGATATTC	240

996

ATTTAGATGT AGGCACCTTT TGTTGTTGGTG GTATTTTCA ACAACTAGAG CAGACTCTAC	300
AATCTTCTTG AAAGATAATG GAGCAGTGGC TTACCACTGA ATGAGTTAGG CAATGCAGAT	360
TTTACCTTTG AAAAAGTGGG AGGCAGGAGT GCAGGGCACT GTAGCACAGA GGGTTAACGCT	420
GnCACTCTGG GATGGCCTAA CATCCCCGAn GTnGATAGCC ACCCTGGGTG TGGAGTCCCC	480
AGGCCTAATT CCTGGAAACC TTTAAAAAAT CCCAnGCTTT nCCCTGGCCT nAAATGGCCA	540
TAATGGGGGG AnGGGGTnGG GGGGTnGGAA TGGGGnCCCC CAAGGGGChA AnCCTGGGGG	600
GGATTAACCT GGG	613

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

TGnGTAATTG CACTAATAGA ATGACCACTT TGTTGTTCT GGTCCTGAC AGAATAGTAC	60
GATAGGTGCT CTTTTGGCAA ATAAAACACT TGCCACTGAA GAAATATTG ATGTTAAGCA	120
ATTTTATTAT ATTTTCTAGT GCCTGGTCCA TACTATGCAT ATAACCAGTA CTTAATGCTC	180
AAAAAAATATT TTTAAATCAA CAGGTCACTA ACTCATTTCT AAAGTTACAT AATTCTGTAT	240
TTTTATAAAA TAGTAACAAG ATAAGTGTAT ATTAAACAGCA CGATATACTC AAGTTCCCTCT	300
TACCTATAAC TGACAACACA CATCCTCAAA TCATGTAACT TTAAGATTCA GCTATTGAAT	360
TAGTAGTGAA AACTTTCCAC AAGTGGAAAT ATTCTTTCA ACTTTGTATT TTTTTAACAG	420
TCTGCCATTC CTAAAGCTGC TGGGTTTGCT TTGCTCCTCC AGTTGGTAAG AATGGAAACA	480
TCAACGATGT CATGGTGTAA ATGAGGAGAT GCACTCTCTA GACTGATGCA GCCTTGCAAG	540
TTAGTGCCTC TGTGTGAAGA GAAAGGCTCT TCTGCCTCTG GGCAGAGACA ACCAAACCCC	600
AGGCTGCATC AGCCCAC	617

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

TTTTAGTTAT TGGGCCATGG GGTGTCATT TTGTTTATT TTTCAAAAAA CCAGCTCCTC	60
GTGTTGGCTGA TTTTTTTGTA ATTTTTTTTG GATTCAATCC TTTTGATTC TTCTCTGATT	120
TTAATTATTT ACCTGGAAGG GAGATACCAT GATCATGGTA GCTTTACTG GTAGATTTT	180
GCCTGCAGCA ATGATTGATG TGGTGCTCCA ATGATAAATT GTATTCCT AATTCTTCT	240
ATATTAATTA GAATGTGTCT GTAAGGAAGA GCTGTGCCTA CTCCACAGTT ATTACTCAA	300
CCACTTATAT CAGTAAGGAC TCCCTGATAT TAATTTTATT GTTCATCAC AACCAAATGC	360
TTTGTACTC ATATTTTGC TCTGATTTT CTCAGTTGGA CCCTCAGGAA CTTTTTTAGA	420
CTTGTCCCTG TGTTCTTCTC ACATCTTCTC AACCCCTTG CCACCACCCAC TACCACCCAC	480
CTTCCAGGCT T	491

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

nACTGAGCTT TTCTTGTAA TTAGCATATA GTTCTACATA GTGGTTTATT ATGACACTTT	60
GTATTGCAGT GGTGTCAGTT GTAATGTTTC TTTGTTCACT AATTTTATT ATTATAGTTT	120
TTTCTTTTT GGTTTGTAG TCATGCTCAA GTTTGTAA TCTTTCAAA ATAATACCTT	180
TTTGCTTTGT TGATCTTTG TATTGCATT TTAGTCATT TCATTTATT CTTTCTCAT	240
CATTATTTCT TGCCTCCTGC TCTTCTGGG TTTGGTTTGT TCTTGTTTT CCAAGTCTTC	300
AAGATGCATC ATTATATCCT AATTGAGAC ATTTCTGTCT CTTTTAACCA TGTAATGCTA	360
TAAACTCCCC TCTACTGTAG CTTTGCTGT ATATCTCAGG TTTGATATG TTATGTTTA	420
ATTTCnCACT TATTCACAA AAGTATATAT TCATTTnAAA TTTCTCAAT GACCTGTTGA	480
TCATTTGGTA G	491

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

TGAGTCCCCA	TGACTCTGCT	TCATGTTCT	TTGGTACTAC	ACTTTCAGAA	CTGTACTGGC	60
AAATGACTTT	GGGGACAGTC	TGTTCTTGCT	CTGTTGCTGC	TCTGAGCCTT	CAATCAAGGT	120
CCACACAAGG	CCAATGATAG	AAATGTTGCA	TCCAGAACAG	CCCCCTTATT	ACTAAGATGA	180
CCTCCAGGCC	CCATAAAATGG	ATCTTGGATC	AGAGGTCAAG	ACTTTCTGTG	CAACTXGAAC	240
ATTTCCTGCC	TTGGGAAGTT	CACTGCnCCC	AnCCCCAGGA	CATGTTCTGA	GCTGCTTGGT	300
CCTAGGTGTA	nAGGCTCTGG	CCGCTGGGAA	TGTTGTACTG	AGTTGACTTC	TGAGTGTCCA	360
GATGCCAGAA	AA					372

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

AGATAGTATT	CAAGCTTCAG	GTAGGTGGGT	TTCAAGCTAT	ACACAAAAAT	AAAGGAGTAT	60
AAAAGTCCTT	CATTTGAGGA	AAAAAGGGCC	TGCTTCACCA	ATTTTTTGTA	GTACAGGTTA	120
GGCAAGATTG	CTTTTTAAAT	TTCAAATGTA	TGACAAATTG	TGAGTTATTC	CCTAATGTCA	180
CCTTATAAAAT	GGATATAGAC	CATTACCTGA	ACATTGTTT	CTTGTGCTTG	GTGAGGCTGT	240
CTTACATGAG	GCAATGAAGG	CTGAGTTCCCT	AATTCCTAA	TCCCAAAAn	nCTTCTTnGC	300
nGCAAGCATA	ACACCAAAC	CGAAGAGTGG	TAAGGTTCAC	AGTTAGATAn	TGCTTGTCTC	360
CTGCATAATT	CCACAGGAGA	GAGAGTAG				388

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

TTTTCTGAAA	TTTAGACCTA	AATAATGATA	ACCAGAAAAA	AACTTTGACA	CCTAAAAGGA	60
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999

TTTTGTAGAT AACACATACTT TTAAAAACTTC ATTATTGATG AACATTAAG CTCAAACTT	120
TGGAAGGACT TGCAACTTAA TGGTGCTTT GCACACTTTT TAATAAATTG CTTTGGTATT	180
TTATGCTTT ATTAGAGGTC GTTTAACCTT TGGTTAAATC GATTGTAGAA AGTCATTGAC	240
ACATATAATC AAAACTTAAC TGTAAAGAGT TAACACATGT AATCAAAACA ACTGCAGATT	300
AATTGTAATG CTGTTACAAA TTTACGTGTT GTAAAATGTC TTATTTCTC TCTTGTATAA	360
TTATTTATAG AATAGATGTT CATATGTTGG CTGTGGTGAA TCGCAAGTAG ATCACAGCAC	420
CATACATTCT CAGGTGTGTA TATATGAATT TTCAATGCAG ACATTTTTA AATGTTTCAT	480
TTTGAGATAA TTGTAAAATG GAAGATGTGT TTTAAAGGG AGACTGAAGG AAAAGGACAG	540
CCAATAATAC AACACTGTTA ATT	563

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

AGGATGGCTG AAGCCCACCTT GTCCATCATA CCAACCAGGA ACTTGGACAC AAGCTGATGT	60
AACCAGACCA GAAGACCAAC CATTGTGACT CCAAGCAGTC CTTTATCACC CCACCAGAGG	120
CAAACATATA GCTGTCTATC CTTTCCCTCT TCTTCCTGAC TTCCCCCTTC TTTATAGCCT	180
CTTTAAAATC CCCCAAATAC CCTCATCCAG GAGGGTGGTA ATTCCCTAAGA CTTTGGTCTG	240
CTACCCCTTC ATCTGGACAA CAGATTAATAA ATTTTCTTTC CACAACCCTC AATCCTCCTC	300
CTGGTTAATT TAATTTGCC ACAAGGGACn GGGACCAAGC TTTGGGGnAA ATCGGAnACC	360
ACTGGTATCT GGACATTCACT CCGATTTTCG TGAGGAGTTG CTGCCGAGTT TGGCTTGAAA	420
ACCAGAGTCT CAGAGTC	437

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

1000	
AAnAACCGCG TTATTTCCC TGTTTCTAG AAGGGGAAGC CGAGGCACAG AGGGGCGGAA	60
CCTTGCCAG AATGGTAGAG TGGGATTCAA AGTAAGGCAG CGCGGCTCCA GAGCCCCGCC	120
CTAAACCACC ACCCAGACGG CCAAACGTCA GACTGACTCG TGCATTCAGA ACTGGCTCAG	180
AAATCCCTTT GTTGGGnGGT AGGGGGGGCA GGGAAAGGCC CACACGCTCT CTGGGACTTT	240
CTATATGGCA AGTGGAnCGG CTGGCCCTGC TTTCTCAGGC AGAGCTGAGC ATTCTGGAAC	300
TCTTGCATTG GGCTGGACTC CAGGAAGGCC TGTGTCCCTG CTAAnCTCCC AGCAGGGTCA	360
GAGCGCACAA CGCTGTGTGT TCCTAGGAnC G	391

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

ACnCCCATTG AATAnGATGC TGGGCCATGG GTTTTCATA AATTGCCTTG ATTGTGTTGA	60
GGAATGTTCC TTCTACACCC AATTGCTTA GAGTTTCAT CATGAACGGG TGGTGTATTT	120
TATCAGATGT TTTCTCTGCA TCTATTGAGA TAATACTATG GTTTTCCTTC TGCACTCTGT	180
TAATGTGGTG TATCACATTG ATTGATCTGT GAACGTTGAA TCATCCCTGC ATACCAGGGA	240
TAAATCCCAC TTGGTCTGGG TGGATGATCT TTCTGATGTG TTGTTGAATT CTGTTGGCCT	300
TATTTTATTG GGGATTTTG TATCTATGTT CATCAGGAAA ATTGGTCTGT AATTCTCTTT	360
CTCTGTTGCA TCTTTTCAG GTTTAGGAAT TAAGGTGATG CTGGCTTCAT TGAAAGAATT	420
TGGGAGGATT CCATCTnTn CAATTGTTT GAATAATTG AGTAAATTG AGTTCTTCTT	480
TAAATGCCTC ATAGAATTCA GCAGTGAATC CATCTGGTCC TGGACTTTTC TTTGTTGGGA	540
GGGCCTTAT nACTGATTCA AATTCTGTCn CAGTTTGGT CTCTT	585

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

1001

GGGGCGTGG nGAACCAC TG GCGCCCTGAC CTGCGGTAC nAAGGAGGGC GAGGGCCACG	60
GACGAGGCGC GGAGGAGCCG CGGAGGGAGC GGGGAGCCCA GGTCCCCCGG CACAGAGCGC	120
AACCTGAGAG CCTGGGCCAG GGGAAAGGGGG TTCATGAGGG GAGAAGAGGG CACAGCCTGG	180
AGCTGGGCTC ACAGACCTGC GCAnGCGAGT CCCCGTGCGA CCACGGCGCC CCGGTCCCAC	240
GCCACGTGCA AGGTGAAGGG AGCCAGGTGC GAGGCCGCGG GGACTCACGG CCCCCGTTCT	300
CCTAAAGTCTG ACAGCAGCTT GGTGGACGCA GCACAGCGGT CAGGGACGCG TGGGACACCC	360
GCCGAGATCC TGGGGGAnCC AGCGGnTCCC TCTCCG	396

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

CCCTCCCTGC CGCCTCGCAG CGAGCTGGGG TGGGAGGCTG AGCAGACGGG ACCCCGGCCC	60
AGCTCTGGCA CAGGAGGTAG GCATCCAAG CGGTGCTTTC GCCACGCCGG ACGCCTGCC	120
ACCCACACAGG TGCGCTTATT CAAGCCGGCC AGTTCCCTCGC CCCGCCGTCT GGCTTCCCCT	180
CTCCAGTCCC AGGAGGnCCGC GCAGGGnCCT GCTCCCGACC CAGAACCTGT CCTAGGTGCT	240
AAGGGGCCCC GGGG	254

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

CCTCTGAGAC AGGAGAGGGC GACTGGGTG GGATGGGGGA GGGCCCCCTG GTGTACCCCTG	60
GGGCCACTGC TGGAGAAATC AGCCCAGGGC TTCTCCCCAG GGCAGATCTG ACCCGGACAG	120
ACCTGAGGGC TCAGCAGGGC CAGCTGCACA CTCACCGCAG GCATAGCCCC ACCCCACCAC	180
CACCATAACAG ACCTGGCAGG ACCCCAGACA CGCCTGCCTT TGTCCCACAA ACATCTGAGT	240
GCCACCGCTCT GTGCCGTGCT GGCTACAAGA GTGGCGGGGA CCTGAGGCTT CTCTGAGGAC	300

1002

CCCTGCGAGT GGACGGAGGC GCGGTCAAGTT CCTGGGGGAA CCACTGCAGG TGGGGCAGAG	360
CCTGGCCTCA TCCAGGGCTC GTCCAGGGCT CAGGGACGCTG TCCGCACGAC GGAGGCAGTT	420
TCGTTCGTAA CCACCGGCAG GCAAGAGGTT CAGGGCGGAA CCAAACTCAG CTCCACCCGC	480
AGCAGACAGA CGGCGTCGCT GGGGCGGAAC ATCAGAGAnG GGCCGCGGAA GGCGGGGGCT	540
CTGGCTGAnG CA	552

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

AGCAAAATAC TTAAGAACTG AAATGAGCAA AAAGCAGTTT TAAGAATATA GGTCAAGGACA	60
TTAATAAAAAA TTTGATCGCC TCCTTTTAT TCTCTAACAT TCCCCACAAT AAATCAGCCC	120
AGTTTCCCCC AGCCCCCTCCT CACACACACT TCACCCCTCCC GTCCTGATTG CGGATCGCAG	180
AATGTAAATC TGTGACAAGG GTATCTATAT ATAATATTAA TGGTGCCGAG GAGGGCTGGT	240
GTGAAGTGTG AGAGCTTGCC AAGAAAGGAG CGATCTGAGC CCAGCCGTTCA ATCCTGCGCA	300
GTGTGCTCTA CATCATCCAC AGGACAAATG TAACATCATT AGGGGAAAA AAAGGAAGAA	360
AGAAAAGGGGG CAGGAGGAGG TAGGGAAGTA GCCATTCTGC AACGAAATGG CCAAGTTGGA	420
G	421

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

GGACTTACTA GATGTGATCA GGATAAAGCT GGATCCATGT CACCCAACAG TAAAAAACTG	60
GAGGAATTTT GCAAGCAAAT GGGGCATGCC CTATGATGAA TTGTGTTCC TGGAACAGAG	120
GCCACAGAGC CCCACCTTGG AGTTCTTGCT CCGGAATAGT CAGAGGACGG TGGGCCAGCT	180
GATGGAGCTC TGCAGGCTCT ACCACAGGGC CGACGTGGAG AAGGTTCTGC GCAGTGGGTA	240

1003

GAAGAGGAAT GGCCCAGCG GGAGCGTnGG AGACTACTCC AGGCACTTCT AGATCCCTCT	300
TCTTCCTTCA TTGGCCTCTC TGGACTTTGA ACAACCACA AGTCAAAGAG GAATGTGAAT	360
CTGTCCTTTT GGAGTGTAGA ATAATGATAT GAAACTGTGG ACATTAGTTT TCCCCAAAGC	420
TGGTGATTTT GTGGAGGGGT AGATTTGTTT TGGTGGTGGA TATTGTTCT TGTTTTTGC	480
ACATCTGTTT TAATTTAATA TTGAATCTGG AGTTGGAAA G	521

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

AGGCACCATT TCATCCCAGA GTCCAAGCTG AGAGCAAAAC GGCCTGAAC T GCACCCCGGG	60
GACAGTTCTC ACTCAAGAAA ACACATTTTC CTCTCCAAC CTAAATTGG AAGGAATATA	120
CTAGGGTTTC TCTAAGCAAA CAAACTTGTAA AAACCATCGG GGGAGGTGAG GCCGCAGGCC	180
CGCTCTACCA GGAGCGCCAT ACCAGCTGCC TCTGGGACCA CCCCATCCTT CAGCTCCCAA	240
GGGGCTGCTT AAAGACTCAA CGTCTCATTC TTCATAAAACC CACCTCCTAG TCATAAGCCT	300
CAGGGGAGAC TTTTTTTAA GCTGGTAGTG ATTCTTGGGC ATAATAATAT ATGACAAAAAA	360
TGAGGGCATG GAGGAGTTAG ATAGAGCTCA GCCAGGTGA AGGTCTTGC ATTCACTCTCC	420
TGCAGCTGTG GCAAAGGAGC AAAGGAAACC AAGCCAGCAA GAGTGTTC GCTGAGCAGA	480
AAAGGAACGG CTCTGACCGG CATGCAAACA CGCCTGCTGA GACCTCCTGC GT	532

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

TTGTTGGCCA ATATAGTTCA GAGGGGTCTG TGTAGGGAA TTTCTGATCC CGACAGGAAA	60
TTCTAGGTCT GTGGCAAAAA GGTTACTACC ACTTTTGTAAC TCCCCAAATC AACTGAAGCC	120
TACCTGGCCA TCATAAACCT TCCCTAAAGG GCACGGCATT CTTGACTAAT CAAGGGAAGG	180

1004

TCACAAGCAC CACTATCAAC CAATAATTTG CACATGAGCT GGACATGAAC TTCTCAGACT	240
CAACTTCAAT CTGTTAAAAC CTTCACCCCT GGAGAGTCTG GGAATTAATC AATAGCTGCA	300
CGGCCTCTTA TTCTGTGCTT TGCAATAAAT GCCTACTCTC TTCCACCATC CGATGCTAGC	360
AATGGCTTCT CAGTTGGGCA ACCAGACCTA GTTTGGGTT CTATAGAAAG TTCTCCAATG	420
AGTTTGGGTT GTCATTGGCA AACAAAGTACT CCAAGGAGCT GACATCTCAT CCACTGGAAC	480
TGAGGGCTCA TGGCATATCA CCAGACCAAG TAAAATGAAA ACGGGGACAG TT	532

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

CAACAAATGC AAATCAATAA AGGCAATACA CCACACCACA TCCACAGAAT AAAGAATAAA	60
AATCACAAGA CCATCTCAAT AGAGGCAGGA AAGGCATTIT ATAAAAATCT AACATCCTAT	120
CATGATTAAA ACTCTTAACA ATTTAAGAAT AGAAAGATAA TACCTCAACA CAATAAAGTT	180
TATATATAAA AAACCAGCAG CTAACATCAT ACTGAATGGA GAAAATCTGA AAGCTTTTA	240
AGATAGGTCA AAAGACAAGA TTCAACATAG TACTGGAAGT CCTAACTAGA ACAGTTAGAC	300
AAGAGAAGGA AACAAAGGTCA TCCAAATTGG AAAGGAGGAA ATTAAATTGT CAATGTTAG	360
GCTGACATGA TCTTATACAA GGAAGAGTCT GGAAAATCTGT TAGAACTAAT AGATTCAAGCA	420
AAGTTGCAGG AC	432

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

TTGGAAGTnA GAGCGnGAGA ACCTGATGTT GGACATGAAT TTTATTTGTC TAATGATCTT	60
CACTCAACTC TCTGAAGGTnA TTTTACCAATT ATCTTACTAT TGTTAATTCT ACAGTCCTTT	120
ATAAAATCCAC ATAAATGACT TTTTCTATT TGGCTGCTTT TAAAATCTAT TTATCTTGT	180

1005

TCTTGCCAAG ACCCTGTACA TCTAAGTACA ATTTTCTCTC TGCTGTCCTA CTTGGGACAG	240
TATGCAACTG TGGATTATG TTTTCATTA GTGCTAAAA AACAGCAGCC ATTTCCCTCTT	300
CTTAAAAGAT TATTCATTCA TTGAAAGGC AAAATGAGAG AGACCAAGAG AGAGAGATGA	360
GAGACAGAAA GAGAGAGATT ATCTCCATCT ACTGGTTCAC TCCCAAGACG GCCACAAGAT	420
GAAGCAAGGC CCCAAAAACT CCAACTGGGT	450

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

TGAATTAGTT GGACAAAGCA AAACAGAAAA ATTCTGGTGG TAATAAGTGA TAAGTCCACT	60
AAGAAAATAA GCAGAGCATA GGTAGGGATG TCTGTGTTAG GGCTGTCAGG GTCTATCCTG	120
CCTCTCTAGG CACTCAAATG TCCGCTAAAT ATGTCTGAGT TGGTTGTTT ATATTATGAT	180
AGAACCTTAT GCTTATCTCT CCTACATACA CATGTAGATA CGAGAATTAT TTATGTGATA	240
GTTCACCCAG TTTTATGATT CAGAAGGTGA CACCTCAGTC TTCCATGTTA ATAATTATTA	300
AAGACTATAT GCCTTAAACA ACCTCAACCT TCCACTGCG AACAGCACAT GTTTGTGGCA	360
TTGATGATT TTCAAAAAGC AGAGGCCCTT TCTTCAGAAA AAGAGAAGAG GCAAATAGAG	420
CTTCATGAAC TAGATTTAAA ATAGGGGCC ATGCTGATAG CCACTGTCAT CATACTGTGC	480
CTTTGGCCA CCAGTCAGAT GCAGGCTCTG AGCTTAGATT CCCTGATTCT AGACTCTGGG	540
GGGACCTCTA AGCCACTGTC AGAATTAGAA ACCAACCTG ACTGAATGCC CAGAGATTAT	600
CCTTAATCTG CTATT	615

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

AGTAAGTTTC AAAATTATGC CAACATGCAG GTCCGTGATT GTCTTGTTC CCTAAAGAAT	60
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1006

ACTGGAAAGGA AGAGGTATTT TTACTTCCTG TAAATTATC TCTTCAGGCC AACAGAAGTA	120
GACCCCTAAA TTCCAAACAG CCCACCCAGA TCACTATTGC TAGAGAATCA CTGGTGAGGT	180
ACTTGTGTCT CCCACCCCCT TTATTCAAG TAGAACAGG ATGATTTTT AAAGAATTTT	240
GCTGGCCTTC TTTCTTAACG GCTTTTTGG CCTTCTCCTG TCCACTTCCT TTTTATTATC	300
CTGCAAAATG ATTATAAACC CACAGAATGT TTTAGACTGG TGAGTGCCTG GAAGGCAGAG	360
CCAGTTCACT AGCCATCCCG GTGAGCCCAG ATGGCCAAC AGGAACGTGT GCTGGAAATG	420
GGCCCAGTT	429

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TTTCCTTCGA CGATGTCATC AGCGTGCCTGCT TTGCTGAAA CACCTCCGTC AATGCCTTGT	60
ACATCATCGA GAATCTGAAA TCCTATCCCA ATAGGCATGA CTTGCGCTCC AAAGGACnGG	120
CCTCACGCGC AGAATAACCT GCACACAAAA ACCCCAAATTG GCCTGATAGA GCGATGAGTG	180
CGCCAGTTTT CAGTGCAACC ATACGCAGAT ACTGCGCAGC CGAGGGAATA AGTTCTGGC	240
TGCGATGCCA TGCAATATCA AGCGCCTGAC CCATATGAAG AGCACCGCTT GCACATTATCG	300
TGGCAGAAAA AAGAGCCGCC TTAAGGGCAG GTTCTATGCT GAGCGTGTCA ATGAGTGCCT	360
GTGGCATGAA AATACAACCA GCTTGCTGGC ATTAAGAACG CAGTCAGTAC CGTAGCGGCA	420
GATACGGCAC AT	432

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

ACGGGACTTA AGGAATGTGA AGTGATCCTA GTTTAGACCA GTCTTGACT TAGCCTCGCC	60
GTAAAGACAG TTCAGGTGCC CACGGCCAC ACTGGAGTAC CTGTATTGAA CTCAGCTCCA	120

1007

GCCCCCTGGCT	CCAGCTTCCC	GCTAATGCGC	ACCTTGGGAG	GCAGCAGTGA	CAGCTCAAGC	180
AGCTGTGTCC	TTGTCACCCA	GGCGGGAGAT	CCAGACTGAG	CTCCCCGCTC	CCAGCTTCAG	240
CCCGAGTGAG	GGCTGTTGTG	GGCATTTGGG	GAGGAAGCCA	GACGATTGGA	GGACACTCAC	300
TTGCCCTTCCA	CCCTTTCTCC	CCCTTCTATT	TCTGATTCCC	AAGTAGGTAA	AATTTAAAAT	360
AAATACATAA	AATACTCCCC	AGAACTAGCT	CCTATTTAA	GTCCAATTAT	TACAATGTCA	420
CAGATACTTA	TCAACAGGTT	AGTCATTCTT	TTCCATTTA	ATAGGAAATG	AAAAGGAAAC	480
TAGGGCAGAA	AAAATTGGTT	TTAAAAGTAT	AGTGATGGGG	GAAGAATGAG	TTTTTCCTGC	540
TCTGCTCTTC	TGAGTACTGA	GGTCATGGG	GGACTTCCAC	ACAGGAGCTG	TGTCTCTGGG	600
TTCACCTCTC	CCCCAGAACCA	CGAGTGACnT	TAAACTGG			638

(2) INFORMATION FOR SEQ ID NO: 493:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

GAATCCCAGG	AGACTACAGT	GAGGACAAGA	GTGACAGTTC	CTCCCCATG	GGCCACCAAT	60
CTGGTGGAGA	GGACAAGAAA	TGAACAAATA	GGGGGCAGCA	TTGTGACCTA	ATGGGTAAAG	120
TCACTGCCTG	CAGCGCTGGC	ATCCCAAATG	GGCACAGCTG	CTCCACTTCT	GATACAGCTC	180
CCTGCTAATG	CTCCTGCCAA	GGCAGCAAAA	GGCGGCCCAT	GGGAAATGAA	CAAATAATCA	240
TTACAAAGCA	TGGCATGTGC	TTTCAAGGAT	TCTGCGAAAG	ATGAAAGTTG	GGGTGGGGGT	300
GCTGGTGCCTC	AGGTGAGCGG	CCAAGGAAGA	AGCCGGATCA	TTTGCTGGCA	CCTGGCCACT	360
GACCTCCTGG	GCCAGGCAGT	ATGTCACACA	CACCCAGGGA	GAAGGGAGGG	GAAGGTGACA	420
TCCAAGGACT	GAGGCAGAGG	GAGAAAGGGG	ACAACCTCAC	TGAGAGGAAC	GGGGCATTGT	480
ATGCTAACAC	AGTATTGTG	AAGCCGAGGG	AGTGGAGGGG	GCTCTGATAA	CTCTCTAAC	540
AAAAGAGCTT	GTCCTGGGCA	CGGGGAAGCC	TCTTCAGTGC	CTGCAGGAGC	CAGCTCTAAC	600
CACCTGGAAA	TCAGTCATGG	GGTGACAGCT	GAGCCCAGGA	G		641

(2) INFORMATION FOR SEQ ID NO: 494:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

ACATCAAGTG ACAGCAGATA AAGCACTTGA CTTTGCTCT TAAACACACA TTCCCTGGGAT	60
GAAAAGAGGC TTAGAAAAGC AGGGCTGGGT CTGTCTGTT TGTCACTGTG TTTACCGTGT	120
GGTCTGCATT CATCAGGGTC TCCCACGTCA GTGTTGGGG TCCTGGCCA GAGAGCAGGA	180
CCAGGAACTG GCTGGGAGTA CACGAGGGGG TGCATGTGCC CGCCCTCATC CAGACGGCAT	240
GAGGTCCACT TGGCTCCTTC CTATCACGAC TCTTCTGGAA GTTCCAGAGG ACGGGGTGGG	300
GGGAGCCGTG GGGGGCTGGG CAGAATAnTG TGCCTCTGGA CAGGAGCACA CAGCAGTTTT	360
CAGGGGGCAA nTGGGAAAGC AAAGTCAATT CTCTGACCCCT GAGGGACTAG CCTCAGTAGC	420
CTCCTATCTT TCCTCCTGAA AAGTTGChAT TCCACCCGTG AGCCTTTCAn CTGTCTTATT	480
TTTCAAAAAA GATTTATTAA TTCACTTGA AAGTCACACT TGAGGAGAGA CAGAGACATC	540
TTTTTGCTGC nTCA	554

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

ACCCCTGCGTC GAAATCAGGA ACCGTCTTGA GCACGCTTGC GCAGGACTTC AACGCTGTAA	60
ACACCTGGAT ACCGCCGACC GTGTTCATCA GATTACTCTC ATCAAAACGC ACCGTAAGCG	120
CGTAGACAGA GTGCTCAGGC GGAACGATCT CGCGCAATTCA CAACCGATCG TATTCAGAAA	180
GAAGAGACAG CGGCGGCACCT CGCCCTACCT GAGGGGCTTC CGTCCCCTCT TCACCTACCG	240
CGGTCCCCTT TGCAAGCTTCG GCTGCATTG GCGAAGACAC CGACAATCCA CGCGCCGCC	300
CCGGCACAGT CCCAGACGCA GGCAGATACG AGCGCAGACG CGCAACGAGA TCCGAGACAT	360
CCTCCCGCGTA GGACCACCGC CGGCACGGGA CTCGAGCATC GCCTTAATTAA CATCCAACGA	420
CGTCAGGAGC AAGTCCACAA CGGCCCCGTC AACAGTTACC TTCTCTGAGC GAATCCCATC	480
CAGCAGATCC TCCACCGCAT GCGTGAAGCC GGACAACCTCG TGCATCTCAA CAGTCGCAGC	540
ACCCCCCTTA AGGGTGTGCC CGCGAGGAAA ATCTCGTCTA CAGC	584

1009

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

AAGTACATTG AATGAAACTT CAGTGACTGC CCAAATGAAA ATAAATCCGC AGTCAGCCCA	60
CCTCCCCACC AAAAAGGAAA AAAAAAACAG GAACCCCGCT GCGATCTTAA CATAAACAAA	120
CAAAACCTCA GAACCGGTTTC TTCAAGCTTC CCAGTCCTAC CnnnnCACCh GCnCCCCCCA	180
TCCCCATAGG TTCATACACC AGCTGCCAGT CCAGTCTTTA AGGATAAnAn ACCACTACAA	240
TGTAGCACTT TCACTTTCAT TTGCTGGGAG AAAGCCACTG GCGTTAAACT GTGGAGAATA	300
TGCCCAATAT GTTTTCCATG TCCTGAGCAA GCAAACAAAG TCTGGCACAC AAATCGGAAA	360
CAGGGAAAAA TGTGAAAATA GCTCAGGACA AATGCTGCCT TTCAGTGGTG TAATCTGCTG	420
CATCATTTAT CTGTCTCTAC CGCTGAGTGT AGGGTTAAA AGTTTCTGAG ACTGGGGGAG	480
GGGAAAATTG ACGCCTTGAA AGTCCAGTCC TAGGTTAACG CCAAGTCAAT TTCCGATGGC	540
CACAACCAAA AAGCGGAATT GGACTTGAAG GAAGGGGG	578

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

GnAGTTATTA ATGTTTTAAT AGTAATAGTG GTATGGTAGT TTTTTTTGTC CTTTTATTTT	60
ATTTTTTTAA GGGAAAGAGT TTATTGGGG AAACCTGACA GACTGGAGGG AAGGGGCAAA	120
AAAGGAAAGA GGGAGAAGGA GAGAAAAGA GAGAGAGAGA GAGAGACAGA GTGTTCAGGA	180
GACGGAGACA AAGAGAGTGT CCTTATATTT TAGAAATGCA GAGAAATAAT GAATGCAATA	240
AAATGATGTC TGAGATGGGC TTTAAAATAA TCTCATGAAG TAGAACAAAT CATAGAAATA	300
TAGATGCAAC AAAATCCACC AATCTTGGC ACTTGGTAAA ACTAAATGAT AGCTACATTG	360
GAGTTCATTA TACCATTTT TTCCTTTGT CTATGTTTA AATTTCTGT AATATTAAGA	420

1010

CATTTACATA TGTATAAGTA TGAAGTTAAA TCAACATTTC ATTTCTCATT CTCATAATTT	480
TTTACTCTTA CTCATAATGT TCTTAATTGT TAGGAAGAGA CAAGGAATT GTGGGAATT	540
TTTCATTACT CTGTTTAGAC GCAGGATGGC ACTCTTGAA TAAGTAATTA GCTAAAGTGA	600
GTAAGTnCCT CTACAGTTC	619

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGGACAGGAT GACAGCATTT CTCCCTGCAT GCAGAAGCCA AAAGTGACTT AAGGAACGTG	60
CCTTAAACAC AGACATAAGC ACAAAAGACAG ATGGTGTAC TTTCTTAATC TGACAACTA	120
CACATAACAA CAGAAATAAA CTCTTCACT CTGTATTGGA GCCTTGGTA AAGCAACCTC	180
CTCTAACCT TAACCAAGAC CTTGGAGAGG CCACTATTAC AGAATGAGTC CCATTGACTC	240
CGCTCACAGA TCTACAGTAG GAATCCTCTA TTAATGAGAA TGTGGTATGG ACTAGATCAC	300
ACAGAACTTG TTGCCTTCAA CTTAACCCCTT CCTCCTGCAA CCCCACAAGC AAGTATTGTT	360
TCAACTTTA AACATAAAGA ACCTCATACC CATAAAAATC AGTGTCTCCC TCAAGGTCAC	420
AGAATTTATT CATACTGAAC TAAATTTAAT TTnnnnTTTT TTTTTTTTTT TTTTTACAAA	480
TCAAACCAGC AATCCTTATT TTAATTCTGT GGTAAATAAG ATTCAAATAA ATTATAATTC	540
TCAACTGAAT AGAATTCA	559

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

CTGnCAAAGA GCTTGTACTG GAAACTTAAT CTCCAAATTC ATCTGAAAT GCTATTTGAA	60
AGTGAGGTCT TTGGGAAATA GGATCACATG AAGTCGGAGA GTAGCACCTC CATGATGATG	120
TCAGTAGGTT CACAAGATGA GGAAGTGAGA CCCAAGTTCG CATGCCTACT CTGTCTCATG	180

1011

TGATGCCTCT GCTGGCCGAT GATAGAAGAA GACTGTCATC AGATGCAACA CCATGCTCTT	240
GGCTACGAAG CCTCCAGAAC TGTGAGCTGA TGAGGCTTCT GTTCTTGTA AATAACTCAG	300
TCTCTGGTTA TTCTGACAAA AAAGTAAATT TCCAGGCTGA TACTGTGGAA ATCTAACAGA	360
TTTTTCGTCT CTTTCTTGCC CTGCCATTGA GAACACATGG GTCTCATGTT GAGATATAAA	420
AGCTTCAAGA TCCAGGTTAC TTGGCTCACT GCATCTCTGT ATGGAGGCCA CCTGCCACGG	480
AGAGTGGCTT GGACCCACTG CCTAACCTTG CATGTGTTTA GTAAAAATGA TGAGAGTACG	540
AGAGACTGTT TAGTCTACCT GAACACAGGC TGCTCTATCT GACACAGAAT GGATGCAGAA	600
ACTGCCCATG TCCAAGTCC	619

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

AACAAACACCA AATTCTGTGCT GAGGTGGAAT AATCGCTTTG GCTTTGTCTC CCGCTTCAGG	60
CCCAGCTTGT GCAAGTCTGC AGAGGCCAGGC CAGAGGGGAG CTGAAATTG GAACCCATGG	120
ATTAAGCAAA CTACGGTCTG AGGGAAAGAGG TTCTTCTAGC AGGGTTTCCC TGGGAAAAAA	180
ATCACCTCAA CCGAGCACCT AAGTCCTGAG TCCTCTAACCA GGAGGCAGCG ATAGAAACCA	240
ACTAAACACC CAAGCCCTCC GAGGGGGGGA TGAACTGGTC ACGAGCATCG CCCCAGCATG	300
CCTGAGGAGA GAGTGACCTC TCTTACCAAT CTGATGGGCT GAGAACTAGG TCCGATGTGG	360
GCATGCAGCG ATGAGATCAG GCAAAGGCTC TGGCTGTGAA TTCGCTCCAA ATGAGAAGTG	420
CAAGAGGGAG TGAGAAAATG TTCTGGAGAG GCGTCTCTCA GGGCCTTCCA GGTCAGAAGG	480
GAAAAAGGAG ATTGTAGGAA AGAGAAGGTT AGGGGTGGGT GGAGACACTA AAAAGGGAA	540
GGATTTGTCC AGATGAAGGG TGGGGGGGTC ACAGCTCTCA CCCAGAGAAT ACGAGATCGG	600
CAGATTGGGA CAAGATGCTG GCCCTTCCCT CTATTTCTCA CACGGGGCAC CAAATATAAG	660
CAAAAGGGTG CAGATCAGAG A	681

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

GGnACAATTA CAGGGGAATG GAGGAAAAAT CAAATTACAT CAAATCCGGT CATTGAGTCA	60
ATTGCTACTT TTCCCCAGGA GGAAATTTTT ATGCCATGAA GTACTAGGGT TGTATAAAAC	120
CTTTCCAGAT CACTTTATAA AACTTGTTTT ATACACTTGT ATTTAGTATT TACATAGTGG	180
ATTCAGCAGA AGGTTGATGT TGACAGTGTC AGTCTGAGAG GACTGACCAG GAnTACTTTT	240
AnTGTTCAGG GAATAGTAAT ACTTACCCCTT ACCCCTTAAC TAATAAGGGG nGGTAATCnT	300
TnTAGTTAGG TTTAAGTTG AGTACCTCTA CTTGGACGAC ACTGGGCACA CTCCTGCGTT	360
TTTGTATATG TTTCTTGGG AGTGTACAG ATTTGACTGA CATCCTGTAT ATATAAATCT	420
TTTAAAACAG TTAGTTAAAT GCTTGGTCAT TAATGCCATA AATTATTAGA TATACTCTTA	480
CTCAACTGGA TGTGCAGTGT CAAGGAGCAG TCATTTGTCA TTATTTGGGA CACTGACACC	540
CAGTCTTGGGA ATATTGGAAT GCCTATTGTC AAGATC	576

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

TCAGCCCGGA GTATGCTAGG TTCACACTCT GGGACTATGA TCCTCAAGGA GTGGGCATTC	60
CAGAGTTGAT GATGATGGTG ACAGTAGTGG TGGTGGTGCC AACGGCATTG CTGTGGGTTT	120
GAGGGGAGTC ACTGTGGGAG GAGTAGTGAT GGTGATGAGG TTTTGCCAAG AAAAGGATGT	180
GAATCAGCGA TGCTTTATTC AAGGAGATAT GAATCAAGTC TGGTCGAGAA AGGTCAACCA	240
CGACAGAAAG TCCAGAAATG TTCGTTCCA AACTCTCCTA AAGTGAAGGT GAAAGCTTAA	300
GAGTGTAAAA TGAAGGGCCT TTATTAGATG ACATCTACGG CATTCTAAA CCTACCCAAA	360
AAACTCATTT TATTTTAAAT TACCATGCTG CCTCTTAAAT TATTTGTGT AATTGTCCTT	420
GTTACCAAAA AAGAATATAA AGACCTTTA AGTTTCTTTA GTTTTAAGAA TGCAAAATTA	480
TATCAGGCTT GATGGAAATG GAAAGTTATA TGCGAGATTAA CTACTCGTAG ATTGCATCTG	540
AGTTTTTTTT GTTTTGTGTTT GTTTTACAT TTCTATCACC TCTCTGCCAT GTAGTGAATT	600

1013

AACATTCCAC CATTTCAGG GAAAGGGATA ATAAGGGTGA AATGTGGGCT GGAATCCnAC	660
CAnCGTGGTA GGAAAATAAT T	681

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

TGATGGTAAT ATGAGAAATG CTGCAAGGTG GAGCGGGCCT GAATCACAGA AAGTGGAAAGC	60
CGGAAAGTAG ACTTATTGAG TTCAGAGAAT GGTTGGCGAT CAGGAAGGGT GATCCAGGAA	120
GGCTTCCTGG GGGAGGAAGG GCTTATTGTT GACCAAGGGA GCCCTCTCAC CATTTCACAG	180
GGTGCTGTGA GATTCAAGAC AGGTTCAAGAG AAATTGCACA TCTATGATAA ACTGGTGAGA	240
TGAACAAGAA CCCAGGGAAAG GCACAAACCTG CAGAGTTGGG GAGGGCGAAG GAGGAGAAAG	300
GATGCTTCCA GGATAGCACT GGCGACTGGA TTGAAATCAC AAACGCAATC ATTCAATGAAC	360
ATTCTATTCC CGGCTTGGAT CAGAGGCACC ACAGAGGCAGC TTGGAAAAGT CAGCTGGAAA	420
GAGAGACCAAG AGAGAGTCAG CTAGAGAGAC TGGACAGAGG TCAAGTGTCA GGCTGCAAGG	480
TAGAGAGAGC TGGAACCTGGC TGCTGGCTTG CCTGCAATTG CAAATGAGCT ATAAAGTAGA	540
GAAGAATCCC CGGATCTTCT CTATCAGGTC CACAAACGTT AGAGGAnCGG CTATGTGACA	600
AGGTCCCTTA CTGGTGGAnA AGAACCTGG	629

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

AGTCTCACCA TGGGTGAAC TCCCTGCATGG AAGTTTAAGC TGAGAAACAG AGAACAGTGT	60
GGCAGCCGGG GTCACAGAAT CCAAACCCAGC AGGTACCAAA GGAGAGAGAT TGTGAAGGCT	120
GAGTGAGGAG AGGGCCTGGC AACATCACAG CCATGGTCAC ACTCATGGTC ATGGTCATGG	180
TCAGGGTCAG ACTGGTTCCA TTTTACTAAC ACAAGAAGAA ATGAAACATA AGCTCCTGCT	240

1014

TCCTTGGTCA GGAGGCAGCT GCTCATCCGG AGGCCATAC TGCCCTCCCC AGCCACCCCTG	300
GCTTCACACC CGTGCCCTCT GTCAATGCTG TCTCTGAGAC AAGCCTCTT CATGGCATCC	360
CTGCAGCCCA TGCTGTCCCC AGGGCCGCCT CAAGACGTAG CCTTCAGCCT GACCTTCCTC	420
CACGCCTCCA GCTACCTCCT GGAAACACTT GGTGCTTCTC GATGTAGATC TGGGGCTGCT	480
GCCAGGCCTA GGCCACCTCC TCGTCCTGGT CATGGACTTG GGGCTTGAT GTCACAGTTA	540
AGGTTAACGCC CAGCCGCTGC CACACATACT TT	572

(2) INFORMATION FOR SEQ ID NO: 505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

AGGGTTACTG TTTTAGGTTA ATGCCCTGTG ATTTTTATGC CCCTTTATGC AAACAGGAAT	60
AGTGTCTGC TTTCAGAGTC TAGAAGAATT GGTTTCTGG CTAGAAACAA GTTGAGGGAT	120
CGGTTAAGGA ATGGGGTGAT CTTCAGATG CCCTTTCCAC ACTGAGAGGA GATTTTGGGT	180
TCCTGAGCAG TGAAATCTCA AATACAGCTT TAATGGGTGT CCATTGTAT GTAACACAGA	240
AGAGAGCTGG CCTTGAAAGA GAGTCATTTT CTTTCACAT TTCTGAGAGA AAATCAACAA	300
CCTCAATTG GCCCAACAAT CATTATGCT GCTTTAATA TATAACAGAC TTTAAGACCA	360
GCACGGGGG TATTCTGATG AATAAACCAC ATTCTCTACT TTTAAGGATA GCCTAGCAGG	420
GGCTAAGTTA TTCATTTAAA TAATTTATGT CTTCATGAAA CTGGAACAT ACAGGGAGAA	480
ATTGCTGGTG GATTAACAGG AATTGACAG GTCAGGATCT GGTTATCAAT CACACTCACG	540
AAAAAGGCAA AAGCAAAGGA TGAGGTTGAC CTCAGTGCCA AGGTCAATTGG ATAGTGAGGG	600
TCATTGGCCC TTAAGCCATA AAAGTG	626

(2) INFORMATION FOR SEQ ID NO: 506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

1015

CAGTGCCTGn	TAAAGAACAC	TAAAGGGTAC	CAAAGCTAAA	TGCAGCAGAA	TTGAAGTTA	60
GCAGATGGAA	GGGCATCTGA	GCCTACACAG	AACGAGCTGT	CCACAAGGTA	TAAGGGTCAG	120
CCGTACAAAA	TACCTTGTGA	GGCTACTACT	GCAAGCATGC	AACCTTCCC	GGAGAGCCCC	180
TCTGAAGTCG	GGGCTCCATT	ATCTCAACTC	TCAAGATCCA	AATCTGGGC	TACATGTCTG	240
ACAACCACAC	TGGCCCCTTC	AGAGAGCCAG	TTATGGCCTC	CAGGGAAGTG	GTGTTAAGGA	300
CCTTCAAATA	AGAGCCTTAG	GATCTCCAGA	ACTACCAAAA	CCTACACTTG	TAGCAGTTGG	360
GAAATTAAAG	AGGTTAACGCA	TTTCTCCTAT	CAGCAATTAA	AATGTTACAC	GAGCAAGGnA	420
AACTCTTAAA	CCTGAATGAG	CCATAAGCAG	ATACAGATCG	CCACAAATCT	ACACCATTCC	480
TGTGACACAA	GTCTATACTC	CTAAGCCCTC	AGAGCAGCCT	CTCTTCTAG	AATATGCAGT	540
CAATnACACA	AAGTGNCTTT	CAATGCTCTT	CCACTCATGC	TGG		583

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

AGAAAACATC	AAAGATATGC	AACTAATGGC	ACTGAAGAGT	TAAGAAGAAA	GTGAAAATT	60
ATGTGTCCAG	GATCTGAGAA	AA GTACAAG	AGGATTATGA	AGACGAACCC	TTGCAGACAG	120
AAGTGGCATT	TGAAACTGCT	TTCTTCCTGG	GAATATCTGC	CAGTCAGCA	AAGAACGGCT	180
GACAGGCTGA	GAGGTGCAGC	TGACAGGGCC	TTGGCAGGTG	GAAACTGGAG	TCAAAAGCCC	240
GCCAAGGGAG	TTGAGCTGGA	AGGAAAGCGA	AAGGGAnAAT	CCCTCTCAGG	AGCTCAATCT	300
GTATCAGGTT	GAAACCTAA	GGGTACACCT	GAAATGGACA	GCCTTCAACA	TGCTGNAGCC	360
CAGCCATAAA	CTTCATAACC	CGGGCAATCA	CACTGAGATG	ACTTGAGCTT	GCTGATGCAC	420
CCAGCAGAAG	TGAAGACATA	TCTTGATTTG	GnAAAGATCT	CAAGTTAAGA	ATATAATAAC	480
CCTTCTAATA	AAAAGTCCAG	CACAGAAGGA	GACAAAAAAAT	GGAACCAAAA	CCCATGAGnA	540
ACAACAGACA	AAAGAGACAG	ACCCAAAAGG	GCTCCAACAA	TGGTnAATAT	CAGGGAACAG	600
ACCTTTG						607

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TGGCTCAGCT GGACTGCCAA GGACTCCCTTG AGCAGCTCAG CTCAGGGCTC AGCCGGGCCA	60
GAATCAGACA TTCAGGTGCC CCTCCCCCG CAAAGTGTCT GGTGTACCCA CGCAGAGGTT	120
ACAATGGAAA TAACCCCGAT CCATGTAGCT TCATATTTAC ATGCACGAGA AGAGAAAATG	180
GCCTCTTTTA TAAGGACATT CATCACAGCA GAATCACCCCT CTGCCGCTTC GCTGTGTTAT	240
TGCTGCTGCT GCCTTGCTGC CGGCCAAGC TGGACTCAGT CTGCCGCTG GCTCACTCAG	300
CGCAGGTCGG CAGGATTG CCGACCGGCT TTGGGATAAT GAGCAGCCAG GCTGTTGGTG	360
AGCAGTCCCAG CAGGTGCAAG AGGCCAGTAG CCTGGTGGGC AGCTTGCTGA GGCCACACCA	420
GGTTTGGCAG GTGCTCAGGG TGAGGACTCT GGGGAACCTT CCCTGGGG	468

(2) INFORMATION FOR SEQ ID NO: 509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

GTCACCAGAT CTACTATATA CGTATTCTT TCTTTCCCCA TTCTTGGTCT GCTCCATCAG	60
CATTTTAACT CCATGGGGGC AGAACGCTGTC TGTTCCATCG ACACCAGCAT CCTCTGCTCA	120
AACTATGCCA GTATAATTG TTGAATGAAT GAAGCCAATA TATTTCTCA AGTATAGAAT	180
CATTTAGATT AAGATAAGGA AATCTTATTG AATATGGAGG TAGAAATCTG GATGAGGCTT	240
TCGTTTACA AAATTATCTC TAACTTAGAT CCATAAGTGG TGTCTGACAT CCCAAGTCAG	300
GAAGCATTCT GTTTAAGGAA ATCCACCCAC ACAGGGCGCC AAGAACCTG GGGCGGGAGA	360
GGGAAGTAGA CTTGCCGTAA AAAGCTGTAC AATGTAAGCA GTAACCTACCA TGCCCCGAAG	420
CCTCAAGTCC CTCAGCTACA AGATGAGCAT CATTACTAAC TCCTGCCCTC CTCTGGGACA	480
GTTCCTnTCG TCATCAAGGG ATCACAAATG TAAGCCCCC TCCTTTTTT TT	532

(2) INFORMATION FOR SEQ ID NO: 510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

GGGTACGCGT CACAGCATT TATTTTGTA AAATGCTCTG CTTAAGGGAT CTAGAGCCCT	60
AAAATTACCA AAAACGTTCA TTGCAAACGT CTCGGGGTGC CTTAAAAGTG CTTCAAGTTCG	120
CCTGATTAA AATCATGGCA TAATTTGATT TTCTCTGTCT CACCATCATT GCAGGGGCAT	180
TGTTAGTATG AAAATGAAGT TTAAAAATAT ACGCTGGAGG AGGTGAGCAC CCTGACAGGC	240
AGAGTTCTGC TCTGTGGTAA GACAGGCCAG GTTGGGATGC ACCGTGTGGC CAGAGTGCTG	300
GATGTGCATC AACCTGTGCA GTGGGGACAG CAAGAGGAAG TGAAATTAAA CGCATAGATA	360
GACGACAAAA CTAATAAAAA CCAAGTGCAT CAAACACAG TGTGAAAGTA AAAATAAAGT	420
GATAGTACAA TCTCGCTATA CACAGAAATT CTAGGAAAGG GAACGGCCAG CCCCTGGTA	480
AAAATTCCCTT TGTTCAAGTCT TCCAGAATGA CAGAATTGT TGAAACATCT TGCCCTTTAT	540
GTGTGGAAT GTAAAAACCT CCATTTTTTC CCATCACCCCT TTGCCTCTCC AnTCCTCTCC	600
TCTTATCTCC TCCAGTCTGG	620

(2) INFORMATION FOR SEQ ID NO: 511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

GGGGTGCTGA GGCACACGCT GGCCTGCTCT AGGCACATGC CCCTGATGGG TCTGTGCAGT	60
ACCATGCACA TCCTCCTAAT GGTGGAGGGA GGACTTGACA GAGGACTGGC AGGGGCAGGT	120
GAGTGTATAC AAACAGAGCT TGGCTCCAAA GTCAGGGCT TGGGTGGAC TCGCCTCCAT	180
GTAATCTCTA AAATATGGTC TTAGGAGGTG AGGAATAAT GCCTAAGTGA TGGGAGAAC	240
CTCTGTAAAC CCAGAAGTGG GGTACACCTA TTGGGAnGGT GGTGGTGGGT GCCCGGAATA	300
AGCTGGTTTC CCAGCAGTGC AGTGGCTCCC ACCCCTCATC CAAGGCTCGC AGGAGTGTCT	360
CTGGGCTGCA TCCTGTGTGG GTCAGGATTG AGCATCGTCC AGCTGTGATC AGGCATCTGG	420
GATGCAGGAG TGAAAGGATA GTCCTTGCCC TCTTGAGCG TCATCGAGAG GGGACAGATA	480

1018

GTGAACAGGC CACTTTAAAG CAGGACAATG TGATGAGGGC CGGTGGAAGT GGGGAAGAC

539

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

GTCTCCCTTG GCAAAGCTGA GGAAGCCTGA TTCCCTCCCC GCTGCCATGC AGAGGTGATG	60
GGGTCGCATG AGGATAGAAA GAGAACATTA TTGGGTTGAT CTGTAAGCTG TTACTCCCCA	120
CTGAAGAACCA GGCCCTGTCC CACTCATGTC TGCCCACCCG CCTTCACCTT ATCACAGCCT	180
TCCACACAGA CGCGGGCCCC TGAGTGGGCC GCTCATGCTC CTAAGCCTGC TGTGAGGGCC	240
TCTCTGATCC CTCCGCCCCCT CACTCTCCTC CTCCCTCCCTC ACCGCACCTG TTTTGGGCAG	300
TGCCAGCTGT GCACTTCTG GACCTGTTGG CTCCCTCCGG CTTTACTCAC ACTTCACCTC	360
CCTGGGGCCCC AGCTCCACGA AGACCTCTCT GCTGAGCCCC CATGATTCT AGGCGTCCCT	420
GCTCCTGTGC TGTCCCCAGG GCCCTACTGG CTCTTTCTTG ACCCCCTCCC TACTGAAGGC	480
AGAGCAGCTG GCAGTTCATC TTTGTCTTTC CCTCCTTTGA CCAGGGCCT AGTGACTCAG	540
AGCCACAGGG CGGTGTTC GGCTGCTGTC AACTGCAGAT GGAGATGTGG AGAACACTGA	600
GGCTGACCAC TGGCCTC	617

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

CCTCTTCTnC ATTCTGCCTG TTCAAGTAAA TAATCATTAA AAATTCCTC TATCAGGGC	60
TGGCACTGTG TCACAGCGGG TTAAAGTCCT AGCCTGAAGC GCCGGCTAGG ACTCGAACCG	120
GTGCCCATAT GGGATGCCAG CACTGCAGGT GGAGGCCTTG CCCACTACGC CACAGTGCCA	180
GCCCTGAAA GTATGTTAAA AGCAGAGTAC ATTTGGGAGG AGTGAGAATG GATCTCAAGA	240
GACAGGTTAA GGCTGTCCTT TTAGGGAGAG CACTTATCCA GGCCAGAGAT GGTGCAGCAT	300

1019

GGACCAGGAT AATGACCACT TACATAGACA GAACCGAGTA ATCAGCATCT ATTCAGAAA	360
CAGAACATC AGGATGTGGT GATGACTTGG TTGTAGGCCT GCAAGAGACA GGGTTGTTGA	420
GGATGCTTCC TAGGTTTCTA GCTTGAACAT TCGAGAGACT ATGATTAAGA GGCCTGTGAG	480
AGGTAAGGGC AGGTGTGTGG AAAATTCAAC CCTTGCAAT AAGCTGCATT TGAAATACTT	540
ACTGAACATC TAAACTGAGA TGGCAAGGAG GCTAATGGAT ATGAGAATGT GTAAATTG	600
AAACAGTCAG CAGATG	616

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

CGGTACACCC ACAATTATTA AATGACATTT TTTTCCAGT GCAGGCTTT GTAGAATTG	60
GGTAGATTCT ATGAATTCCC AGACATCATA CTATGACCAC TATATGTATG TGTGTTCATA	120
ATCACATGTG TGTGTGTGCA TGTTACTTG TAGAGGGAGA ATACATAGCT TTTCTCAATA	180
AAATGCATAT TGCAACAGAA GAAGGGCCAA AGCCGTATTG GCCTCAAGGC AGCGTGATCT	240
ACTAGAACTA AGCCTCACCA AGAGGTTGAG AGATTTGTGC CTTTGTGTCT CCAGGGGACCA	300
CTAAGCAATT GTTTGACTCT AGGCAAGTTA CCTAATCTCT TCATATCTCA GTTTCTCAA	360
CCATGAAATG GAGGAAATAA TACCCCTGCAC CTGCCCTGTTT CAGCTCATAG GGCTATGGTG	420
AGGATCAAAT AAGGAATGGT AAGGAAAAAC TTTGCACTGA AGAGTTCTAC ATATGCATGG	480
TTTAGGAGAT TAGGCTCTCC TGCTCTTCCC CACACCCCCC TCACCTTGCC CACCCCTCAA	540
AACTCCCTGT GAGAGAACCC GGCTCTCACT TTCAGGGAAT TTCCTCACTT CAAAGTAAAT	600
AATTATCAAT ATnTnCTAAA TTTTACATT TCTCAGTTAT CAGGAAATGT TATTTAGGGC	660
TCTGCCATA	670

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

CTATCCTACC TATCAGTAGT ACAATGAGGC ATTGCCAAA AATGTTGGAG GAACAGATCT	60
CAAGGGAGAG TACCCCAAAC CTTCTGCTGA TTGGTAGTTA TAAAGTCATTT AGATAGTACG	120
GTTGGGGAG GTGACAGAAC TCTGAGCCCT CAAGTCTAAA CCATGGCAG TGAAAAATCC	180
CATGTGAAGG ATTTTAGCCA CTCTATCTTG CTGGAGAGGC TTCTAATCTT CCCCCACCCC	240
TTATCCACTA ACACCACAAA CACCAATT TAATTTCTT ACTAGTAGAG GACCCTAATT	300
AGGCTCTAAT TAGCATATGA ATAGAGGAAA CAAGAAGGGA GACTGCTTT AGTGCTGGAA	360
GCTGCTATCC CAGTGATCTC TTAATACTTC CTGATGCTAG AAAATCCCTG GAAAACAAGA	420
ACACAAGGAT TAGGCCACAC TAGCCCATT CAGGGCAGGT TAAAATAATC AAGGTAAGCA	480
ATGTGCTTCT TCCCTTAGCT ATACAATTGAT ATTATCT TGGAGTGCTT TTACTTACAA	540
TTGAATATAT ATATATnTGT GTGTACTGGT GCTGTTAGAC TAGGACTGAA CATAAGTTTC	600
TCAAACAGAn GCATGTTGCA AAAAATCTCT AAGGAATC	638

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

GTCTGATCAA AAAAATAAAA TTAAAAAAA TAAAAAAAGAA TGCATACTAT GAAAAGCTAT	60
GCATAATTTC AATATTTTTT GCACAAAAAA ATAAGTTTAT CCTTAATTCC TATATTCCAC	120
TTTCCACAG ACATTTGGC ATGCCCTCAT GTAACtgaca GAATCCTAAC TGTGCTCATA	180
GCACCATATT ACTGCTTGCA ACAAGCAATT AGTAGCAACG GTGCTGGAGT GCAGCATTAA	240
GCCAATCCCT GCACTCTATA AAAAGTTAAA GGGCACATGC CCAAGCAGGC CCCTACATGG	300
GCACAGATGC CTGAGAGGGG AGAATTGTAC CGACACAACt CTGACCCCTCC AGACCTCCCA	360
AAAGGCAGGG TGGGGCAGAA ACCGGCTCCA CTTAGGAGGA AGATCAACTA CCTTCTCTTA	420
CACCATGGTG AAGAAAGTAT AGGAGGCTGC AGACTGTTG CCTGCCATAC TTTCACGTTT	480
CAAAAGAT GAAnAACCATC AAGCCTGGGG GAGAGAGGTG CTCAGCAAAT CGGGTGnAAT	540
TAAGAGCAGA GACGTCTGCC CAGCTGTGGG CACTCA	576

(2) INFORMATION FOR SEQ ID NO: 517:

1021

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

CCACCCGTGT TCTTAAATTT TTCTTGATTT CCTAATTATC TATTTTGCTT TTGGGCTTCT	60
CTTTTCCATC ACTTACCATA ATATTGAGAA TTTAAAAAAA ATTAGAAAGC AGGAAGCTGG	120
AATCAGGAGT GGAGCTGTAT TTTTTTTAA GGTTTATGTA TACACACACA CACACACACA	180
CACACACGGC GGGTGGGAG AGAAACTCAG AGTTGGACCA GGCTAAAGCA AGGAGCATGG	240
AACTCCTTCC AGTCTCCCCA TGTGGATGGG CAAGCGTCCA AGCGCTCAGA CCATTTCTG	300
CTGGTTTCC AGGTGCATCA GCAAGGAGCC GTATGGATG TGGAGCAGCC GGAACCTCAA	360
CCAAAGTTCA TACGGATGTG TAGGCAGTGG CTTCATCTGC CGTGACATAG GCCAGCACCT	420
GGAGCTGGGA CTTGAACAC ACATCCAAG CAGCATCTTA ACTTCTACAC CAAACGCCTG	480
CCCCCTTTAT GGnTTCTTTG TTAATTGTCT GAAAGATACC TGAAGGGTGC GTTCCATCAC	540
AGATGTGGTA TTACAATGAA TCCTCTGAG GGATATCAn ATTTTTT	587

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

AATGATGGTG TAGGTCCGTT CAAAAATCTT ATGCCACAAA CAAAACACAG CTCTAATTAG	60
TATGTGATCA TAAACAAGGT AAACGCACCT CCCTAAAGCT GTCTTAAAGC CTTTGTG	120
GTCACCTAGC TCAGAGAGAC GCTCTGAATT CTGTCTCCAT GCACGTGACC AGGGCAAAGA	180
TGTGGCATTG TCCAAATCTC ATCAAGAGGA TATATCTACT GTAAGGnAAG AnTGTCTGC	240
AAAAAA	246

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1022

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

TGTGCCGGCA	CCCGGCGCCG	CnGGAAGnGG	ATTAGCCTAG	TGAGCCGCGG	CACCGGCCCA	60
TAGTTCCCTA	TTTTTGAAATG	GGAATGATAA	GTACCCATCT	GATAGGGCTT	TTGTGAGGAT	120
GAAAAGAGTT	GGAAATATTA	AATCATTACT	TAGGGGCTGA	CACTTTTTT	TCTTTTATGA	180
GTTGTTTATT	CCAAAGACAG	ACTGACAGAG	AGGGTAGAGA	GAGAGTGAGG	TAGAGAGAGA	240
TCTTCCATTC	GCTGTTTCAT	TCACCAGATC	ACCACAACAG	GCTGGACTCA	GTCAGGCCAA	300
AACCAGAACG	CAGGAACATGC	AGCCAGATCT	CTCACATGGG	TTCAGAACCC	CAAACAGTTG	360
GGCCATCTTC	TCTTGCCCTTC	CCAAGCACAT	TAGCAGGGAG	TTGGATCAGA	AGTGAAGCAC	420
CTGGGGACTC	CAGCCGGCAC	TCGTATGTAG	TGCTGGCATT	GTGGTTAGTG	GCTCAACGTG	480
TGCTGCAGCG	CCAGCCT					497

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

AGCGATGATA	TTTTCTTCAG	CGCGTGCCT	ACGChnCCC	ATTCTGCTGA	TCTTCAAACT	60
GCGCAAAAGA	ACTCATCGCA	GATGAGTnAC	AACTCGTCCA	ATTTACTCAG	ATAATAGCTG	120
TCACGTTCTG	TCAAACAGTC	ATCAAGAAC	TTTGCCTCCG	TGATCACTCT	GCGCGCCGTC	180
TGCCCTTCCA	TATAAACTCC	TCATCCCCA	ATTCACGTC	CTCGCGCGTG	TGCTATACCC	240
TACACCACTT	AnAGCGTGAG	AGAAAGCTTA	TACGCAGCAC	GCCGCGCGTA	CTCAAACGCA	300
GGACACTTTT	CTGCAAGGTT	GTAATACATA	TCACGCGCCT	GGGCGTGCAA	ACCCTTTTG	360
TATAAGAGAT	CTGCAAAATG	GAGCAGTGTC	TGCCACACTC	CATGCTChTG	CGCCCACCTTC	420
AAAAATAGTCG	GATGAGATCC	AGTCGAAA	AATAAATCAG	CAAGATCCTA	TACTGATA	478

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1023

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CCCGTTAAGG CCAGCTCCCG TTCAGTCCTC ACATCTGGGG AGGGTCACCA CCAAACTCGGG	60
AGAAAGTTCTA CTTAACATCC AGCTTGTAAC CTTACTGCTA TTACGTTCA TGTCCACTGT	120
CTTGATTCTG GATAAGGACC CTTAGAGCAT TAGAAGAGGA CAGCTGTCCC GATGGGCACA	180
CCAGGCTGTC CTCCCTCTGT ATAACCTGGCA GCTTCTAAGA GCTATGCCCT ACGCCCAGGG	240
AGGGGCCTGG CAAGTGGTGG GCACCAATGT ATGTTGAAAT AATGAACGTG ACTGCATGCC	300
TCCTCTCTGG GCACGCCTGG CTTCTCTCAG GCCTCAGTCC CGGGCCCTTT CCTTAGGCCAC	360
AGGTTGGCTC TTCCACCCCG GACATAGCAC AGCACGTTCC CCTTCCCTGT CTAGTCCTGA	420
GCTGAGGACG TGGGAAACGG GGCCCAGGTT AGGCATCCAC ACCTCCCATG TCAGACTGAA	480
GCTGTTACAG TGTCATCTCA GGGACTGCTT CCCTGTGCTT AGTCCTTAGG TACCAAGGGG	540
GCCTACGTCT GGGAGAGGAG AAGCCAAGA GTCCCCAGCT TGGGGTGCCT TGGGCCCCGTG	600
GAAACCCCGG CCCACCTGCA GGGAAGCGAT GCTGAAGCCC TGAGCGC	647

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

GAAGCAGAGG TGCAGTGTCC CGGAGCCCTG CCCGCCCTTG TGGGCCTCTA ACACTAGCTC	60
CTGTCGGC CCACCTAGAG CGCCCTGCGG TTGGAGGACG GAGACCTGGA GGAAGCCGCA	120
GCTGCTGCAG CTGCAGGTGG GCGGCGGGAG CGACGGAAGC CGTCTTCAGA GGAGGGCAAG	180
AGGAGCCGCA GATCTCTGGA AGGGGGGGC TGTGCTGTGC GTGCCCCAGA ACCTGGGTAA	240
GCATGCATCC GGGTAGATGC GGAGGGGTTG GATCCGCCAG GCGGGTGGCC CTGCGCTCTG	300
ACAGGCCCCG CCTCCAGCCC CACAGGTCCC GCCTCCCCGA CAGGCTCCTC CTCCCTCCGTC	360
ACGAGCCCCG CCCCGCTGGC CGGCCCCGGCT TCCAGCCCTG TGAGCCCTGT GAGCCCTACC	420
TCTGGCCTCC GTACCTCCGT GAACTCTTTC CTACCATTTC CACGGCGCCG TCAGGG	476

(2) INFORMATION FOR SEQ ID NO: 523:

1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TAGTATAAGC CAGAAAAGAA CCCAGAACTG AGAACCCACT TTGCAGACGC TAAATTTAGA	60
ACTGCCTGAG GCAGCCTCTT TCAGTCAACT TTCGGGTAAA TTTTCTATGG CAAAAATATG	120
TGCATTGATT AGACTTTTA ATCCATCCGA GAGCAAACAG TGCTGACACC TTGACTACCG	180
GGGTCCCTCAT CCCTAGCCTG CGTTGACAGC CTTAGGCTCG TGTTCCCATA ATGTACTCAA	240
ATCACACGCT TCCGGGCTGC GAACTACAAA CCCCAGCATG CATCACTTC A TCTTCCACAG	300
GGGnGGGGGG GGCGCCTGCC GGGGACTGTA GGCAGCCGCC GCTCTGGTGA GTCCAGCCAG	360
GGACAAGAGC CTTTGGGGGA CACGTCCCAA ACGGGCCAGC TGCGGACTCG GAATCCCGTT	420
TGGCCGCCGC CCTGCTCCTG GCAnCCGCAA CCTCCGACAA nCGCACCCCC AGCGGCG	477

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

nCCGGGCGAn CTCGAGCGCG AACAGGCGGC CCAGGCCGCT GCCGGCGCCC GTGATGAGGC	60
AGACCTGGCC GGCCACGCTC TTCTCCTTGG GCCGCACCAAG CCAGCGCGCC GCGGnCCAGC	120
ACGAATGCCAC ACAGCACTTT AAAAGTGACC ACGAAGAACT CCACCACGAT GTTCATCGCG	180
ACGCCCAAGGT CCCCGnGCCA GTGCAGCGCC CGCGTCCGCA CCCAnCCCGC GCCGGGCAGC	240
CCGGCTCACC GCCCCGGGGC GCTTGT	266

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

TGCCAGTGCC TACTGCTCCA TCTGGTGCAG AGTCTTCCC CAGCTACCTT TTGATTTCATG	60
CTTTTAGACC ATTCAGGTAG CGCCACTAGA AATTATTTCC TGTCTTCCTG TTCCCTCCCT	120
GACAGCCGGC AGCTTCCCCC TGTGGCGTTC TCTGTAGTTT TTATCACGGC ACTTCACATT	180
CATTTTATAT ATATCTTGCC TTCATCATCA AACCCGTCTT GGTTTCACCA AGACCTAAC	240
CAGTGCTCGA CAATGACAAT GAATGTGTAT AAATGAATGT CGCAGGGACT GGCCTTTGT	300
CCTnAGGTTA AGATGCTGGT GTCCCATAACG GGAGTGCCTG AGTTTGCTGC CGGCTCTGGC	360
TCCTGATTCC AGCTTCTCAC CAATGGCAGC TGCTGAGAGG CAGTAGTGAG AGGCTGTAGT	420
GATTGAGTCC CTGGCCACAC ACAGGAGACC GGGATTACGC CTCTGCCCTCC GAACTTCAGC	480
TTGGCCCATT CTGGGACATT GTGAGCATTT AGGGAGTGAA CTGGTGGATG GAAGTGTGCA	540
CACACTCTCT TTTTCTCTCT GCTTCTCTGG TGGCCnCTCC TCCCCTT	587

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

TTGAAAAAGC CAGGAGAGAA TGCTGGCTTA GAGTTTCTCT TATCATCAAA AGAGCAAGGA	60
CGAGGGCTCC CCTCGCGTTG CCTGGGGATT GTGTGGCTGG AATCCAACCC CTACTCCTGT	120
CTCTTTTACC AGCATCAAAA GAGGAAACAC TTGCTTTCAT TTCAGCTTTC CTAGATGTGA	180
GGCCAAAGGA GTGAGAGTGG GGAAGAGGGA AGGGATTGAA AATTAACAAAC TGTTAGTAGT	240
GAAACATCGG ATGGGATGCG ACTCTTTATT ATAATTCTTG AATATTATTT CTTTTGCC	300
GTTGAAATA CTTTTTCATA ATTTTATATT TGGATTGTTT ATTGTGAATA TATAGAAAGT	360
CACTTGATTT TTGTATGTTG CATTTCATTG TGCACCTTGC AAAGATCTT TATTGGTTCT	420
AAGAGTTTT CAGTGAACCTT TTTTGGGATT CCTATATACA AGACCATGTC TTCTGCAAAG	480
AGAAAGTTTT GCTTTTTGTT TCTGGGnTTC ATACTTTAA TTTTCnTGCC TAATTGCTGT	540
GACTAGAACCA TCACAGACCA T	561

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs

1026

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

CTCGCCGTCT AAATCCCACA GGAACCGACT GTGTCCCAGG CACCCCTGCA GGGCTCTGAG	60
GGTCCTGATC TCTTCCTGGG ACCCCCACAC CTCCAGCGC CAGGGAGAGG CCAGGAAGGA	120
GGGAGGAGCT CAGGGACGGG GTCCATCCCT GGCTGCGGT GGGACCCCGC CCAGCATGGA	180
CGCCATGGCC AGCCCGGCAG TCACGGGGTG CTGCTCCCCG AATCCTGGGC CACCA _n CCCG	240
TCTCCCCCA CnCCTCTTCT CCCCCACATC CCTACTGCAA GGCCCCGGGA GGGGCACACC	300
CTGGGGAGTT CAGAGGATGG ACAGCAGGTG GCCCAGTGGC TCCCAGGGAT AAAGGG _n AGC	360
TnGGCGTGGT CGGA	374

(2) INFORMATION FOR SEQ ID NO: 528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

GTGCACATTCTCTATTCACT TTAGATCACC TCTAGATCAC TTACAATACA TCACAGAATA	60
TAACATATAAA CAAGTAGCTG TATTGTTTAG GGAATAATGA CAGGGAAAAA ACACGTTTAG	120
TACAGATGCA ACTTTTTTTC CCCTAGATAT TCTTAACCCA AGGTTAGTTG AGCCATAGAT	180
GTGGAATTCA CAGAAACTGA AAGCTGACTG CAATCAGTTC TTGCTAACAG GGCTGCCCT	240
CAGAAGAACC TAGTTAATCA GAGAAAATC TGTTCTAGGG GTATTCTAAG AGCATAACTG	300
ACAGAGAGAA GGGAAATACC CAAATCTAGT TAGCTCTAGT CATCCTGTCT CACCTAATCT	360
GGGACAAAAT ACTGACAAAC AACTGTGAAT ATCCTCTTCC AAGAACATT AAGTCCGAGA	420
TCTAATCAGA GTAGTATAAA ATACTTACCC TGTCACTAAA GGACTATTTA CATAATTCCC	480
TTTACCTGT AACATCACAT CCAACTAGCA AGAAGAAATT ACAGGGCTGA CATTGTGACA	540
TTATGGATTA AGCCACCACT TGTG	564

(2) INFORMATION FOR SEQ ID NO: 529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs

1027

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

CGGATGCAGC TTGTTCCCTCT GCATGACGGA TGAATTGATG GTGCAGCCAG CCTCTTCCCT	60
GAAATGATAG GCCACTGTCT CCAGAGAAGC TTGTCTATGA GTGGCACTCC ATATCATCCC	120
CAGCTACTTT TGAGATTAAT GTGACAATGT GTCTTGCTT CTTCTCAATG AATTCCAGCA	180
CTGTAAGTnT GTnTAGCTCT CCTAGTATCT GGAGCTGCAG ATTTCTGCAG CTCTGGGTAT	240
GTGGAGGACA CCCCTGCCTT CAGCAGGACC GAGTTAGGGC TGGGGCTGG AGGTCAGGGA	300
GTATATTTC AGTAGCCCCA TAGCAGGATG TTAATTACA AACAGCTGGA ACTTTCTCGG	360
GGAGCACAGG GGCATCTGTT TAGGGCAAGG ACACCGTATG TGTGTGAGGC TAGAGAAAGG	420
GCGGCTGGTG GCAGGAGCAT GGTGATTGGG TATA GTGTTG CTGATACAGG CTTGTGCAGA	480
GAGGGCTGCC CGCCCTGGC CAGATGCAGC CTGTAGCTGG TGCATCCC	528

(2) INFORMATION FOR SEQ ID NO: 530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

TTTTGTTTTTC AAAATGGAAA TGTTCCTTAG GGGTTTTGGC ATGCTTTTG ATATGTTGAA	60
AGATGAGAAA ACATCATTG GAAACTCAGC ACTTATACCA TATTAGGAAA TTTGCAGTGC	120
CTCAGATTTC ACATTTAATG TTTTAATTGC CTGGTTTGGG AATAGAAAAC TTTCAAGCTT	180
CTCTCTTCA TTTCGAATTT CCACTGCTAA CTTCCCCCTC TGCAGTGGTG GGCTGCTGCC	240
TGCCCCATTT CCTGCCCTGG TTCCAGCATG GACCAGTGGT TGCGAGAAAG CAGTTCATCG	300
CATGTCATCT GAAATGAATA TCATATTGAC TTCCGACAGA CTGGCTTACT CTTTTTTTGT	360
GATACCACAC ATGCAGTTGT TTCCGTGAGG ACTTGAAAT ATCCTAAAAG TGCAAC	416

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1028

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

TGCACACGTA TGGGCCGCC	CAACACAGCC	GCCATGACAT	TAAGTGTCTA	GAGGGAATAG	60
ACACAGGTGA ACACATGTGG	GCCGCCAAC	ACAGAGACAC	AGCCGCCATG	ACAGCGTGTG	120
TCAGGGAGGG AACAGACACA	CGTGACACAG	TnGnGACCAC	CCCAACACAG	CCGCTATGAC	180
AGCGTGTGTC AGGGAGGGAA	TAGACACAGG	TGAACACGTG	TGGGCCGCC	CACACAGAGA	240
CACAGCCGCC	ATGACAGCGT	GTGTCAGGGA	GGGAACAGAC	ACACGTnCAC	300
CGCCCCACAC	AGTAGACnCA	GCCGCCATGG	ACA		333

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

AAATACTCGA CATATTAAA	AAGTCTTTTC	ATTTCATTC	AAAATAACAG	TCTCTACCTA	60
CTCATGAGCT TCCCAGGTT	AAGACTTAAC	AACATTTGG	AAGACTACTG	TGAACCTCAG	120
CTAGCTTAC TAAGATGTTT	ATGTGTTGTT	TGGATTAATT	TTGACCAAAG	ACCTGTATGA	180
AGTTCAAGGC TGATCCTCTT	ATGATGACGG	TCATTTCTGA	GCCAGCCTGT	TATGATTTG	240
TACTTATCTC AAGTGTAACT	TTACTACTTT	CTATAACGAG	CAGAGTCCAA	ATGCTTGGCG	300
CTTGTGTTAGA GCTTTGTGCT	GCCTCAACCA	TCCACCGCTA	ATTCAGATAA	TTTGTTCAGA	360
GAGGTTAGAC GGCCATCAAC	TCCATAGAAAG	CTCCTCCGGT	CCCCCCAGAT	CACAGAATT	420
TGGCTTGCAC TTCTAGAAAC	TGCCAGGGC	CTGGCACACA	GTAGGCAC	TT ATTGTTAA	480
TGTTGTTGG GAAGGAAGTA	GAGAGGCAAG	GAGGGAGTTG	GCAAGGGAGG	GTGATGTGGG	540
AAGCCGTCT GAAAGAGCCC	ATTCTGACCA	TGGCCGTGTC	TGAATCGTAG	ATTACAGCAG	600
AGAACGCGCG	TGGATC				616

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1029

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

CATCTTGTC CCTCTGACTT GTCAGTCTGT CCAGGGGCC ACATCTGAGC TTGTAAATTA	60
CCACTCTACC CTCTCTTCCC TTTCTGCCAC CAACACCCCTT GCTCTCTCCT CCCAGCCCTG	120
TGTGGGGAGC CAGGCTGGC ACCTCCCAGA AAGGCTATTG GCTGTTGGCT GCTCTCTGCC	180
CAGGCATCTC TGGGCAGCCC AGCATTGGCT TCTGCTGCCCT CCTGGAGGTG GAAGCTCCTG	240
GGTCCGTGTC CTGCCTGGTT GGACCCGTGA ACAAGCCAGT CCCTGTGAGG GTCTTCCCTT	300
GGCAGGCCTC TGGCTGGAA GAGGACTCTT GGCAGAGTCC ATGAGCTACC CTCGCTGGAA	360
CTTGAAATTC CTGCCAGAA GGGGATGGCC CAAAGCTGCA GGAAGTACCA GGTGCAGCGG	420
GGCCCCCTGGG TACCAAGGATG CCACTCCCCT GCCATCTGCC TTCCCCGTCT GACCCTGCTT	480
CTCTGCTGGA ATGTTGCCTT CAGTTTTCA GACAGCCCTC TTCACACGTA TGCTAGAAC	540
ATCTTCCCTG GGGGTCTCAC AGTTGCATCT TCTTCCTCA _n TCCAATTCA GAAAATCCCA	600
GGGGAGCTTC TCATTGGTC CATTAGGGC CCATAnA	637

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

TTCTACAAGT CCGGCACGTT CCGTTATGAG GATGTGCTCT GGCCGGACTG ACCAGCGACG	60
AGACGAAAAA ACGGACCGCG TTTGCCGAA CGAATACAGC ATCGTTAAC TTTACCCCTTC	120
ATCACTAAAG GCCGCCTGTG CGCTTTTTT ACGGGATTTT TTTATGTCGA TGTACACAAC	180
CGCCCAACTG CTGGCGGCAA ATGAGCAGAA ATTTAAGTTT GATCCGCTGT TTCTGCGTCT	240
CTTTTTCCGT GAGAGCTATC CCTTCACCAAC GGAGAAAAGTC TATCTCTCAC AAATTCCGGG	300
ACTGGTAAAC ATGGCGCTGT ACGTTTCGCC GATTGTTCC GGTGAGGTTA TCCGTTCCCG	360
TGGCGGCTCC ACCTCTGAAT TTACGCCGGG ATATGTCAAG CCGAAGCATG AAGTGAATCC	420
GCAGATGACC CTGCGTCGCC TGCCGGATGA AGATCCGAG AATCTGGCGG ACCCGGCTTA	480
CCGCCGCCGT CGCATCATCA TGCAGAACAT GCGTGACGAA GAGCTGGCCA TTGCTCAGGT	540

1030

CGAAGAGATG CAGGCAGTTT CTGCCGTGCT TAAGGGCAAA TACACCATGA CCCGTGAAGC	600
CTTCGATCCG GTTGAG	616

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

CCCTGGTCTC ACTCTGTTA TGGAAACCAG CATTTCCTCC TCCCTTGTGT TGTTTCCCTT	60
CCTCCCTTCA TTCTTCCCT CCCTCTCTCT CCTCTTCTG TCACTCTATC TTTCAAATAA	120
ATTTTAAAAA ATGTTTAAAA GGAATACTTC TGTAAGGATG TCTGTCCAAC ACCTGCGTAA	180
CCATGTACTG GTGCCATCTT TGTTACTGAT CCTTTAGCAC ACTTGTACC AACCTTGTG	240
GTCAAAGATT GTTGTGTCAA AACAACTTAT GTAACCTTCC CCACGTTGTC TTTAAAACA	300
CCCTTGCCT CAGCTTTAT GAATATACTC ATAGTTACA GTGACACAGG TGCCCCCATT	360
GCAATGTCAT GTGATTCTCA GACAAACTTT TTGAATTTG GAGAAACTGT CTTTGTAGGT	420
TATTTAGATC GACAAAGTTT ATTCTGCTAT GATTTGTATT CTTTTAAATT TGThAAGTTT	480
TAATGGCCA GAATATGGTC TATCTGATG CATGGGCACC TAAAATTTG AATTGTGCGA	540
nCTC	544

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

TTTCTAACCC CTCTTATCC ATATCTACCC CTCAACCTTT CTGAACCAGT CTTGAGTTCT	60
AGCAGTCACG TTCTCTTGTGTT TTAGTCCTCC ATGATGTGCT TTCTGACTGG AACGTTCTCT	120
GCATTGTCTT TCTTCAGACC TCAGCTTCCC CACCCCTTCC ATGAGAAAAC TGGTGCTTTA	180
CACTCTCCCC ACTGCATAAT GCTTGCTTGA ACCTCCTCCT AGCTTCTACT GAGTGATTGT	240
GTCCTGGTCA TATGTGAATG TCTAGTTAGT GCCTAGCACA ATACTTTCA TGTAGTAAAC	300

1031

CATCTGTGAA	TGTTGGTTA	AACGAGTTTC	TGACAGTTT	TTTGAGTAC	TCTTCCAAGG	360
CCTAGTTTC	TTGTTGTGG	GAAGTCACC	AGAAGAGTAG	GAGTTGGAAG	CAGGCAGACA	420
AGAAAAGGTT	CTTACTGGCT	CCAGCTTGC	ATGCATTTT	TTTCCCTCT	TCATTTCTT	480
CTTCCATAGC	ACCGTTCAA	TTTCAATCA	TTTTACTACA	CTAGTCTCA	CAGACCTTCC	540
AGGCACAGAT	AAAGCTAAC	GAGTTTAAG	GCAAATGGTC	GGTCCTGCA	CCCAGCTGTT	600
AAGAGGGCTG	CAGAGTGTGA	GTGAAGACAG	CTGAAGTGGn	TAACTAATCA	AAGGGnATCA	660
TTCCCTCTGG	CAGGACA					677

(2) INFORMATION FOR SEQ ID NO: 537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

AATTCCCGGC	TTCAGCTGCT	AGGGCATT	GAGGGAGTGA	ACCAGCGGAT	GAGAGCTCCA	60
TCTTCATCTC	GATTCTCTC	CCTCTTACAA	TTAAATTTT	TTAAAGGTA	ATTGATCATT	120
GTTCTGTATT	TCTTTGGTT	ACAGGTGTT	TTAAGTTCAA	GAGATTTTT	AAAAAGTAGA	180
TACTGCAACA	CGTATTTTA	CTACGTTCGC	GACTATTTTC	TTAACAAAGAG	CCATCTGCCA	240
CTGATTAAG	ATCTTCATG	CATTATAATT	ATTGCAAGGG	ACTTCCCCAA	TAAGCTTAGA	300
AAAGGTGTTG	TGACTTCTGC	CGTCTGCATA	AAAGCGGGAG	AACGAAGCCT	CAGACGCATG	360
AACCGACGCG	GCCAAGTCAC	AGGTGCAGGA	GAGGTGTGGA	TTCTCATTCC	GGCGCCCGC	420
CCCACCGCGA	CTCCTGCGGA	GGCTCTCTC	ACCCCAGCAG	AGCCACCATT	AGCTCGCCGG	480
GCAGCGTCCG	GGCCAGGTT	AGCCGCGCG	CCCCCGTGAG	GCTGACGCGC	TTGGTTGTTA	540
TGACGACACG	AAGGGCAAAA	GCCCCGGAA	AAGAACTTG	AAGGGCATTA	GCGGAAAGCG	600
CTCCCCACCC	CAGGT					615

(2) INFORMATION FOR SEQ ID NO: 538:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

TGAGTTAAC	AAATCTCTTG	TCTATAAGGT	TGGCCTGCCT	CGGTTATTC	ATTATATCAG	60
TAACACACTG	ACTAATGCAT	ATACGCAGAT	ACAGGACTGC	TGGGTCATGT	AGGAATTGCA	120
GCTGTAATCC	TCTGGGGAGC	TGCCATGCTG	TTTCCACAC	AGCTGCAACA	GTTCGGCGA	180
TGTACCAAGG	GTCCCATTTC	TCCCCATCGG	CGCCAACACT	TGCTGTTTC	CGTTTGTCTG	240
TCTGTAGGGG	CCATCTGCAT	GAGTGTAAAGT	AGACCCTCAG	TGTGGTGATT	TGCACTTCTT	300
TATGATTAGT	AAGTTTTTT	CATGTTTAA	AATTTATAT	ACTTGGTGGT	CATTTGCATA	360
TCTTCTGTAG	GGAAAATATC	TATTCAAGTC	CTTTGCCAT	TTAAAAACCT	AGATTATGTT	420
GTTGTTGTTG	CnATATAAGA	GTCCTTTATG	CATTCTGGAT	ATTGATCCCT	TATGAGATAC	480
ATGATTTCTA	AGTACTTTCT	CACATTATTC	AGGTTACCTT	TTCTTTCTT	TTTAGAAGTT	540
ATTnATTTAn						550

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

CATTTATTTG	GTATGTCATT	TTCCCCCATG	TGCTTGCTGC	ACTACCCTTG	CTACTCCATC	60
CCTTAAATCA	CAAACACATA	TGTACCTGCA	TCCATCCCCA	CTCACATTAT	ATTCACATT	120
TACTTCCATC	CACCAATGC	TCGATTCTGT	TAATTAGTT	TTTAAAGAT	GAATACTACT	180
GAAATTCTTG	TTAAGTCTTC	TAGCAAACTA	TCAGAAGCCC	TAAGGACAAT	GAACTTGTTT	240
CCCTGAACTG	ACAAACCTCA	ACTGAAGCTG	CACTAGAGTC	AGCTCCTTTA	AGGTGTGACC	300
ACTTCATTCA	TCCATGTTGT	CTGGCTGGCC	CTTGGACATA	TTAAATTTTT	TTTTACTATC	360
ACTCTTCACT	TGTTTGTATC	TTGACCTGTC	AACACTTCAT	TGGAAAGTTG	GTAAGGAAnC	420
AAACCAAAAA	AAACATGGTA	GGTAAGTATC	CCCACCAA			458

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

CAAAAGTACA GGAGGAGTAG AGGGACGATG ATCTGTCTTT AGAGTTACTT CCTGCTGACA	60
TGGGGCAATG AGGTACTCTT CATTGGCATG GGGTAATGTC TCGAGCAGCT GTCTCCTGGG	120
TTGGGAGCCG AGTATATCCC TGTAGCAGCA TTTGGTTGAC TGCGCTGGTTG CTGAAGGCCT	180
TGGTTAGCTC CATTATCAAC TCTTTAACAC ACTTAAACAG ACATGGTAGT TTAAAAGACA	240
GGGTGAGAAT AGCAACAAAT GATCCTAAGA GTGGCATTAA CCCGGTAATA AGAGGATTTC	300
ACAGAGGAGA GGAAACGAGG GGGGTGGTCT CTGGACCCCT GTGATGACTG TTTGATGGTT	360
TAAAGCTTAT CTCACCCAAG ACTGGGAGAA AGGCCACTCA ACTTTGCAA GTAGAGGGGT	420
TTGTCTGTAG AGAAATTCTG AACAAATCATT CAACATTA	458

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

AGGGCATGAA AGGCTGTTCC GGCCACAAAA TAGAGACCCT GTTTAAATCT TATTAAACAA	60
TAACGCCCCAC CCAGTCCTCC CCTCCCCCCC TTTGGAAAAA AATTCAAGAA GGAAATTGTG	120
GTTAAATCAT CTCATAGTTT GGCAAAAACT TCTACCTCTG AAAAATGAAA AGAAAAAAA	180
AAACTCCATT CTGTGCTGGA CTCACACAGG CTAATAAAAA GCAGGACTGT ATTGCTTTGC	240
ACTGTAGCTG TCAAATTCTC AGCAATGAAA TACAGACCCT GACTCTCTCA GTCCCTTGCG	300
TCCTACCCCC TCAGACCACC AAAAAAGGAA TGGCGGGGGT GGGGGATGGG GTATCATTAA	360
TCCTCTCCCA TTCTAGAGGG AATCTTGTCT GTnGCTTTGT TTCACTTTA ATTTCTTGGT	420
TTGAGGTCCA AACATCTCCT TTCCCTGAATA AAGTTTCCAC TGTTGTTATA AACATACATA	480
TGCAAGGGGT GTTGGGAGCT GGTGCTCTGA AGATCTGTGC TTCTGCTGTC TTGTAGAGAT	540
ACCACACACT TGCCATCAGA GAAGAATGGA CATTGCAACA ATGAGAAAGA AAGAGAGGAA	600
GTAGAGAAGG GGGGAnAGAG GGAGGGAGGG AAGGAGGGAG GGAAnG	645

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs

1034

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

CAGCCAGGTA	ACGAGTAGTG	CTTTTGGTG	TGTGGCAGTA	AGATGAGTTA	TTCTGGGATC	60
CCAGTTCTGG	TTTGGAGTGA	CAGGAGACCC	TAGAGTCCC	GAAGCAGCTG	GTCAATTAG	120
CAGATGTTTG	TACCTCAACC	AATTTGAAAT	GGATTTGGCA	ATACAAGGTG	AACAGTGTAG	180
TCACATGTCT	TGTCTCTCCA	TTGGGACATC	ACAGGGTGCC	CCCTAGGGAC	CCGTTGAGCC	240
CTGGAGAGAA	AGCTGGTGGT	GATAAGGCTG	ACCATGCAAG	GGAGGGCTGG	CAGGCACAGC	300
CGCCCTAGGG	AAGGCAGGGA	GAGGAGGCAC	CTGTTCTGGG	CCAGACATCC	CACTGCTAGA	360
TCATCTCATC	CATTCCGGAG	CTGATTGGC	CCTATCCCC	GGAAGATGGA	AGTACGCC	420
AGAGAGCGCA	TGGCAGAGCC	TGGATGTCCA	TGCCAAGTCC	AAATCTAAA	TCGTTCACAG	480
ACTAGCTACA	CGACACTGGG	CGAGGGTGTC	CTTCTCCGTG	AAACCAGGAC	AGTGAGACCC	540
TCCCTTGTA	ACCATACAGC	AGCCGTGGGG	CTCGAAGGCC	ACTGCTGTCA	GAGCCAGTGC	600
CCTCCAGGGT	GGCGACTCCT	AGGGAAAGGTC	CCAGCCTCAG	GCTGTGCCAA	GTGCACCTGC	660
TTCTCACCTG	CAAAATTGAC	C				681

(2) INFORMATION FOR SEQ ID NO: 543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

AGTAAATCTG	TATTTGAAGG	TGAGTCTGAA	TTAACACTGT	CTTCCTTTA	GGGCTTGATC	60
TCAGCAGTCA	GATCAAGGGC	TGTCTTGTGA	CTGCATCAGC	AGACAAATAC	GTGAAGATCT	120
GGGACATACT	GGGAGACAGG	CCGAGTCTGG	TTCATTCCCG	GGACATGAAA	ATGGTAAGAA	180
TCTCCCTGAG	TCTCTTAGTT	TTCTGTTTT	CACCTGTGTC	GCTTGTCA	CTCGGGGAAT	240
CAGTGCAGTA	AAGAATGTGG	ACAAGTGGG	AAGTTAATTG	TGGTGGGAGG	TTTAGGGGCC	300
TCAGACCATT	CTGGGAGAAG	AGAGACTCGG	AGGGTCAGTT	TCTACTTCAC	ACGAGTAACA	360
GCTGTCGAGT	AAGGAGGGGG	CGAGGGCTTC	TCTAGGACAC	AGGTGAAGTG	GCCATTGTCT	420

1035

CACCCTAGGA AATCCTGATG CTTAGAAAGA ACCAGGAATT TTTCTGTATT GAACACCTGT	480
TGTGTACCAAG GCACTGAGCT TGATAGATCA CAGAACACCA CATAGCTGTT GAAAATCATG	540
TACCTGTGTA TTn	553

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CCTTTTCACA AAAAGCAGTC CTTATCACGG GGTGCGTATT CTTGTGCACC CCTGTGTCAT	60
CCGCACATGA TGACCCAGCA GTTGGTACAT GGTAAGTATG ACCAATACAA TCTGCAAAGT	120
GAGTCCGGGG TGATGCTGAG TCATAACCCCT CCAAAAAAAG CTGATCTCTG CAAATTGGAC	180
CCTCGTTAC CTGGAAGTAA TAATCTGGCT TTGCAAGGCT GCACAGCATA GTAAGTAACA	240
ACCCCTGTAG CATTCCGGTTC TCATATCAAT CAGACTGGAG GGTAAGATTG TCTACCTTGC	300
TCGTCACTGG ATTCCCTCTA AGGGCCTTGC AACAGATTG TCAGATGAAA GGGTGAGCGA	360
GCAACCAGCA GAAAGGCACA GGATGGGATC ATTGTTAACCA GCACCGACCT GGCCTGGTT	420
TTGTGGTGCA GTGGGTTAACG CCACCACCTG TAACACCGGC AACCCAGAGG AACACGGGTT	480
CAAGTCCGAG CTGCTCCACT TCCAATCCAT CCCTATTAAT GTAGAGGATG GGGGTCCCAG	540
CCATCCAnAA GAGAA	555

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AACTCTGCCT TTCCAATAAA TAAATCTTTT TTTTTTTAAT TAAAACCCAG AAACCTGGCA	60
CCCTCAGTGA TTGAGAAACT TTACCTGAAT GCTTTTGGC ACGTTCCCTTC ATGATCCAAC	120
CACCTGGACA AAACCCATTC TATGTGGTCT CAGGTGAGCT TGAAACTGTA ATGGnAGAGA	180
GGTCCACTAT GTGGCCTTGT TCAGTCCTCC TTTCTCTCCT CACCGCTCAT GTTTCAAAAG	240

1036

ATAGATATCT ATTTCCAAGA TCTTGGAGG AAACCATAA GATCAGGGAA AACATAACAG	300
CAAAAGTTCT GTACCCCTCCC TGGATGGTTT TCTCCCCAAC ACCATCCATG GGCGAGAGGC	360
ACAGAAATGG TTCCCTACTG GTATTGCCA TGGCTCCTG GAAGCCATCT TGGAAAGGGGA	420
CTAGAACAAA CACATTTTA GCCCCTCAT A TCCAGCATCA AAAGGAAAAC CCAAGTAAAC	480
AATTAAATAA TCCTGGCATG GTGAGGGATAT ACGGAGTCAC TTGGGTGAAC CTGGAGTGGA	540
CTATCTGTCG AGCT	554

(2) INFORMATION FOR SEQ ID NO: 546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

ATCCTGAAGA ATAATTGATT TGTAAATAGA AGCACTCAAT GCCTCAATCC CTAAATCTAC	60
TATGTCAAGA CATATTTCCA AAGTTGATTT TGTGAAGGTC CTTACAGAAAT ATGTAACATT	120
AGCTCTCCTC AGGTAGCCAT TTGGTTCTGC AACACACTCC TCAAAACCTA TTTTACTACT	180
GACTACTACT GCTGACATTC TCAACTCACA CAAATAGTTC AAAAAGCAGT GCTATGTAAA	240
ACTTTCAAA AAGTGTATTA AATAGTTCA TCACACTTCA TTTTGCCAAAC CAGGTGAATG	300
AAGCAATTTC CCTCAAAGGA CTTAAATTTT TAACAAAAGG TCAACTCTAG AATTTCAGATA	360
TAGTGAGTTG AAGCATCAAC TTGCCTCCTG TAAACCACTT ATATTCTTAA TTTTCATTGT	420
TCTTTAAATT CTTTAGTTAT TTCACTTGAA AGGCAGATGG ACAGTGAGGG GTGCGGTAGG	480
GGTGGCAGGG AGGGAGTGGT TTCCAACTGC TGCTCCATTG TGTAAACGCT TACAACAACC	540
AGGGTTGGGC CAGGGT	556

(2) INFORMATION FOR SEQ ID NO: 547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

AATCGTTGAT CAGATCGCGA ATAACGCTTC GGGAGATTTC TTGCGCCGGGA TACACTGAAA	60
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1037

TCCAGTGCTT TTTATTCATG TGATAACCTG GCTTAATGCT TGGGTATATT TGCTGATTAA	120
ACAGGGATTT TTGTGGATCG GACTTCAGAT TGATAAAGGG GACGCCGC GT ACTCCGACGA	180
CAGCATAAAA ATCTTGCCGC CAATTTTAAA AACATCGAAC TCCGGGCCAA AAGGCCAGCA	240
AAGCTCGACA AAGGGTAACT CAAGGGCCAG GCGTTTCGCG TTTCGTGCAG TGATTGCTTA	300
TCCATAAACG TTCCTTTAGG CGAAGGAGAA TAAGCAAAGT ATGCCGCAGA GTACGGCGAT	360
AATCGACGTT TAATCCGCCA GCGAGAACCA GCGTCGCCAG ATAAAGCGCA GAACAAAATA	420
CTCAATAGCG CCCAGCACTA AAAACCACAG ACAAAACAAT AAAGTGTAAA GCTGACTAAG	480
ATCCATCAGA TGGAACATGG TCACCAAGTT TTGTGCCAGC GCCAGCCCCA GTGCGGGGGC	540
GGGCAGCAGC AG	552

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

GGGTGAGCGC TTTGTGCCA CTACCCACAC TAACGCCTAC TTTTGATTTT AATGCCAGTT	60
TAATGTAGGG GTGAATCTCT TTCTTTGGGA TAATTCAAAA AATGCATTAA CCTGGCCCTT	120
GGGGTACGGC ATTTGGGACA TCAAATGCTC CACTGCGTAG TCTCTCTGCC CTCAGCGAAG	180
TCTTCATCGT TGTCTCAGTC ACAGTGCTCC TGTGGGCCCT CCCTGGTCCG CTGTCGGTGC	240
AATGCGCTGT AGTTTGGGG AGGAGTCGTT GTGAATGGAA AGGAAGCGTT GGATGGGCAG	300
TCATGTACAG AAGGTGACTG TTGCAAGGAC AGCGTACTGG ACACATAACG ATGTGTGTGG	360
GCTTGGGCAG AACCAAGGCCA GGCTGTTGAA GCAAGTAGAG TGGCTATTT TCCCCTAAGG	420
GGCAACTGGG GGCCnAAnTG GTT	443

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

1038

AAAGCTCTAC ATCTAGCTAG TTGGTAAGAG TATTCTTTGG GACAGATGAT GGGCAAGATG	60
GAGATAGCAA GTATGAATCA GCACAAAAGT CTGGGTGCAC TTAGAAAAAT GAGCACAAAT	120
CACATATTTT GTTAATATTT TGTCAGTATC TTTTTATTTA TATAAACAAAT TGTATATAATG	180
AGTAAATCCA GTTCAACCAT TGACATTCTA TCTAAATATT TTCCAGGTTG CCTAACCCAC	240
AATTCTATTG CCATGGCAAAT ATGTGTTCAC CCAACATTTC TGAGCATGCT TTGATTTTC	300
TGGGCCCTGC AATTTCCTTC ATTTGAAAAT CTTCTTGCCC CCTTTAAATA TCCAATTAT	360
TTATATGAAC TGTCTCTGAA GCCTCCCCA ATAATCACAC TGGAGTGTGT CCCTAGACTT	420
CTACAATATT TTGTTGAAG CAGTCATTCA ACATTTATGT GACATAATAT TTCACTTAAG	480
TTGTGTGTGT AAATATTCAA ATTTCCTAC CCTATTCAA TCTCTGAAA AGTAAGGAGA	540
ATAGATTAAn AATATTATAA ACnTTATAGC TGCATAGCG	579

(2) INFORMATION FOR SEQ ID NO: 550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

TGTATCGCTG TTCAGATCAG TGCCTCTGAG GGGACATGGT CTCTGCAGCT TCTCATTGGT	60
CACTATCTGC TCCTGTCTCT TCAAGGGTGA TTTTAAATGC AGAGCAAGGT TATAACAGCTT	120
CCATTTACAA TTTTACAGG GAATGCAATG AATCAAAAAG AAATAATCCA GAAGAGGAAA	180
ATCTGTATGG TTTTACATAG GCAATTAGAC CTTCTCCAAT TTTGTTCAGC ATGCTTCAAA	240
TGGAAATCTT AGCAACAATT TCAAGTGGAA ATCTCAGCCG TGAACACTAA GTTCTTTCA	300
CAAAAATAGA TACAGATTTT TCAAACATCA ATATGAAAACA TTTTTAAATA TAGAAATAAA	360
GTACTGAAAG TATTTAGAAA AAAACAAGCA AAATATTGCC TATTCAGTTA TAAATACAGT	420
GCCAGTTGTG ACCCTTTATG GTCTGGAGAA TTTTTTTCT ATGGATAAAA TTGTAATATT	480
AGGACAGATT GTCAATTCACT CGGTCCAAT CTGATTTATT TTCACTTCA AAAAATTAA	540
AACATTGTTT AAAATATATG CnACATATAA GGChAGACTA ATGGTATA	588

(2) INFORMATION FOR SEQ ID NO: 551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1039

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

nAGAACGTAG GATACTGATT CGTTTCAGAC GGATGCGCGC ACAGGGAGCG TCTATGCACA	60
GCTTGTCCGT GCGCCGCGCG TTGCAGGATT GCTGCTGAAC ATAGATATTC CCTCTCTCCC	120
TGACGGGTAC TCTTTTTATA CTGCAGCACA TATTCCCGGA TGCAATGCCG TTCGGTGTGG	180
GGAAAATACT GTGCCGGTTT TTGCCCATGG AGAGGTGGTG TACGCAGGGG AACCGGTGGG	240
TATCCTCATT GGGCCTGATG AGCATGTGGT ACGTAATTAA GTGCAAGATG TGGTGGTGCA	300
TACGTGCGCA GAGCGGGCCT GTGCGTCGGA AATACTCTGT GGAATCAGTG AAGGGGAACC	360
CCTCGCTCAA AAGGTGGCGG TGCAAGGAGA TGCAGAAACT GCTTTAAAC GCGCATCACAA	420
CACGGTATGC TCCTCTTGTA CATTGAGCC GCGTGTACAC TACTTTGCCG AAATGCCAGA	480
AGTACAGGCA CTACCCGACG CGCACGGTCT GCACGTGTAC GCTGCTACGC ATGGCCTGCG	540
CACATGAGAA AAACTATCGC GCAGGTACTG AATATTCTG AGCATGCGGT GCACGTACAT	600
CCGCAGCAGG AAGCGCTTTC CTGTGATGGG AGAATATGGT TCCCCTCAGT GATGGCAAGT	660
CAGGCAGGCGC TTGnAnCCTA TTGTGCGAAA AAGCCGGTAC	700

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

CACGTTGCAG GAAGAAGATC AGCTGCTTGC AAGCAGGTCA TCGTGCAGCG CanATGTGGT	60
TTTCTGTACA CCACACGTGT TCTACCATGC ACTGTGCTCG AAACCTGGCGT GGTCAAGGGAG	120
TATTTTTCT CGCAGGGAA GACGTACGA TGATTGAGCA ACTTTCGGTG CGCAACGTTG	180
CGCTCATTCA ATCTTGCGC TTGGAGTTTG GTGCACAGTT TACTGCCCTC TCAGGGGAGA	240
CGGGTGCAGG TAAGTCAATG ATACTCGGCG CGCTGTCCCTT TCTCTGTGGG CAAAAGGTAG	300
GGCCTGATCT TATTCGCAAG GATGAGAACG AGGCATGGGT TTCTGCGGTG TTTCGCTGTG	360
ATCACGCACC GCTGCGTGCA CACATGGTTG GCAGAACGGA GTATTGAGCC TGAGCACCAC	420
CGCGTGCTCC TTGCGCGGT GATGCGCGT ACCGGTCGTG GCACGGCGTG GATTCAAAAC	480

1040

GTCCGGTCT CTCGCGAAT TTGGAGTTT TCACGTCATT TTCATAGACC TCCACGGACA	540
GCATGAACAC CAATC	555

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

CAATCCATCT GAACACCTGC ACCCCACGAA AGCGCTCAGC AAACGCACAC ACCTTCTGGA	60
TTTCTTCTGG CAAAAGCCCC GAAAGGGCGC ACACCACTCC ATATA CGCTC CACCCCCTCG	120
TCGCAAAGTC CTGCACCACC TCCGACGAAG AGGAGGACCC CGACCACAC ACAAAAAGCG	180
CCGAATCGAC AGGCATCGCG CAnCCACACC TGCGAACGGA GCCGTTACAA CTTGGCAAAC	240
GCCACCCATA CCCAAGCTTA CCAGGAAGAA AAAGGGGGGA AACTACGATG CACCCCTCAA	300
CTTCACTCAT AAGCTCAGAA ACAACACGGT TCTTAACCCC AACTGCTGA AAGGGACGAA	360
TGTCCTTCAAG CGCCTTTTGC TTCTGCCGA GCTTGCGGTG GCAGTCTTGC AAGCTCCACA	420
TATACGCGAT AGTTTTTCCG ATTCAAGCTG CACGAGTCGA TTCAAGACTC ACAACCGGCT	480
TCTCGTATC TCCCCTGGAG TTTACAAAGG ACTGCGAGCC CGAGCGTGGC ATAGGCATCG	540
TAATCGATAT CCAA	554

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

CAGCATGGTG CGnTGAATGT GTTCCCCGGG CnTTGTACAC ACCGCCGTC ACACCACCG	60
AAGTTGGAGA TACCCGAAGT CACTAGCCTA ACCCGCAAGG GAGGGCGGTG CCGAAGGTAT	120
GTTTGGTAAG GAGGGTGAAG TCGTAACAAG GTAGCCGTAC CGGAAGGTGC GGCTGGATCA	180
CCTCCTTCT AAGAGAAAGG GTATGGCAT GGCATGGTGC CGTGTTCGnC GTGTGGCGGA	240
AGCCACACGG TAGGTTTTC TGCTCctGCA CGGCAGTCTC TCCCCTTCCC TTTTGAAAAG	300

1041

GGGCTTGTAG CTCAGTTGGT TAGAGCACTT CTCTGATAAG GAAGGGTCA TTAGTTCAAC	360
TCTAATCAAG CCCACTATTA TTCTTTATGT CCCTTTGTPT TGTTTATGGG GTAAGGAGTA	420
GGTGGTAGGT GATTTTTGAG AGTATTAGGG TGGGGTGTGA AGTGAGAAG GGATGGATAAA	480
TATGGTCAAG CGAACATGTGG TTTACGGTGG ATGTCTTGGA GTGTCAGGC GATGAAGGTC	540
GTGATAAGCT GCGAAAAGCC TCGGGGAGGA GCACATGTCC TGTGATCCGG GGATGACCGA	600
ATGGGGTAAC CCGACAGGGT AAAGCCTTGT CATTGCCTTC CTGAATGAAT AGGGAGGGTA	660
AGGCAGAAACT GGGTGAACGT AACCATCTAA GTAACTTGGG AAAAGAAATC AAGAGAGATT	720
CCGAAAGTAG TGGCGAGCGA ATTGGAGGA GCCTAAACCT GTGTCTAACAA GGGGTTGTAG	780
GGCCGCGCGG GCTTGCCTTC GGTGGGTGAA ATAATCCGGC CTATAGCAGA AAGGTTTTGG	840
GAAAGCCTGA CAGAGAGGGT GAAATCCCCG TATGCGGAAT GGGGCGGACC TGCTGGTGCG	900
GTACCTGAGT AACGGCGGGA CACGA	925

(2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 940 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

TCTGGGCTCG GACGGTACAG TAGGCGCGAA TAAAAATTCA ATTAAGATTA TTGGTGAGGC	60
GACGGATAAT AACGCGCAGG CTTACTTTGC CTACGATAGC AAGAAGTCTG GTGGTTTTAC	120
TATTTCTCAT TTGGCTTTG GAAACAGAA GATCCGTAAG CCCTACCTCA TTACGCAGCG	180
GATTTTGTAG CGTGTCAAA GTTACGTAC CTTGAAACCT TTGACATGCT CAAACGCTC	240
AAGCGTGGAG GGACCTTTT GCTGAATGCG CCGTACAGTG ACCATGAGGT GTGGCATCAC	300
ATACCCATAG AAGTCCACCG TCAGATCATT GAAAAGGAGG TGAAGTTTA CGTCATCGAT	360
GCGATTTCTA TCGCTCAGAA GGCGGGATG GGCACACGTA TCAATGTGGT GATGCAAACG	420
GCTTTTCAA AATTTTGTT ATCTgCCGGA AGCTGAGGCG ATTGACCTGA TTAAGAAATT	480
TATACAGAAG GCCTACGGCA AAAAGGgTGG GGAGGTTGTA CAGAGGAACA TCACCACTAT	540
CGATATGGCG CTCGCTGGGG TGGGATTGGT GGAGTATCCG GGAGTTGCCG GTAGTTGGT	600
GACGCGTCGT CCTGCGATGA GTTCCGATGC TCCGGAGTTT GTGCAAAGCG TGTTAGGTAC	660
TATTGCGCTC AATCAGGGGG ATAGTCTTGG GGTGAGCGCA CTACCAAGAGG ATGGTACCTA	720

1042

TCCTACTGGT ACCACGCATA CGAGAAGCGC TGTATAGCCG AGACTATACC CAT ^T GGGATC	780
CGTCTGTTG TATCCATGTG GTCATGCGCT AGGTGTGTCC TCACGCCATTA TCCGCATGAA	840
AGCGTACGAT GGTAAGGAGC TCGAGCAGCG CCTTCTAAGT TTGCTTCCTG TGGA ^T ACCAA	900
AGGCAAGGAA TTGGGGAAAGC GAATTACGA TTCAGTTCC	940

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

ACAACCACTG CCACGATGCG CCCTGCCTTG TCCACAAACAT AAGTAGTTGG CAGACCACGG	60
GAAGCAAAAA CACTCCCCAA ACTCCCCTCC TCGTCAAGAT AGATAGGAAA GGTATGCTTT	120
CCACGCGCGA TAAAACTTTC CACCTGTTT CTCGAGTCAC CAACGTTGAC CGCGACAATC	180
TGAAAGTCAT TCCCCCTCAT AAGAGCCTGC ATGCGATCCA TAGACGGCAT CTCCGCACGA	240
CAGGGCGGAC ACCACGTAGC CCAAAAGTTC AAAACCGTCA CCTTTCCCTT GAAAAGGCTA	300
GGAACCACTG CCTCCCCCTT CAGGCCCTCG CATGAAAGTC ACTAGAAAGG TCGAGCGGGT	360
TTGGGATACA CAAAAAAACG GAAACGCTCG AGCGCCTTTC AGCGAGCGGG AAGGTACATC	420
CGCATTGTGC GCCACATCGG CGGCTTGTAC GCnGGAAACA CCCCACACCG CAGCACCCAGG	480
ACGGAAGGAA CACAAGGGGA CGCGCGTAAA GCAnCGGTAG TACGGGAGCA ACTCATGCAC	540
AGGGAACATT CACT	554

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

GCGTCAAGCA CCGGGAAGCG CACTACGCTC CAATATCTAT TAAAAGATTT TGTACCTCGT	60
CCCGGACAAA TGTGGGATAT AGCGTATGCA TACAATTTTG TGCATCCGCA CGnAACCGCA	120
GTGCnTGCAG TTTCCGGCGG GAGAAGGGAT GCCTTTGCT ACGGCGTTGA GGAGATCGGT	180

1043	
TAACGCTATT CTCAAATACAG CACAGGATAT TGTGAAAAGT GATGCCTTCT TACGTGAGCG	240
GCGCACATTG CTGGCTGATA TTGAAACACG TGAGnTGCTG AGCTTTACG TATTGAAGCG	300
GAGTTGTATA CGCGTGGTT TCGTGTGAGA TGGCATAGGA AACGTGGTAC GTACTCCTTT	360
GATTAGTTC CCCTATTAAA GGGAAAAGAC AGTAGCTTTG AAGCGCTGCA CGATTTAGCT	420
TCCCGCGCGA AnTTTACTAG ATGTGTAGTA CACGAACCTCC ATGCGCGATA TCGTCTTTCC	480
TGTGATGAGG TTTCTTCGCT GCTCCATACG TTGCGCACnG CGGGGCGGGC CGCCGTAAGG	540
CGTCTTGCAG AnTACTACCG TGCGCGTTTG CGG	573

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

TGGGCTGCTC TACCGGAGAG AAAGAGATGG AAAAGGCTGC AGACATCATT CGCATGTACG	60
TTACCGACAC GCTTTCTTCT GTGCGAACAT TTAGGCAGGA GTCACACACG CGCGCAACCT	120
ACGGCTTTTG CACAGAGGCT CACGGTACAG ATACCTCTTC AACGATAGAT TTTTCACAAC	180
TGGTGTTCAC CGCAGAACAG GTACGCCACCA TTGAAATCGC GAAAACATT ATTACAAAATTG	240
AAGATCGGGT ACTTGGTGTAT GCAATCAAAT ACTGGCACAG ATACGATGAT CGAGCCTTTG	300
AGAACACCGT GCTACTGTAC AGCAGAAAAGT ATAAAACACA TCACTACAAT ATCTTCATTC	360
AATTAAAACG GGACGGGTCA CCAATGGAAA GACGAnGATA TTTTGCACTG GTGCTCGCGC	420
ACGTCGCCTC AGGTATACTA CAGCATCAGT GGTGATCTGT ATTGCAACGA AACGGCACGG	480
TTAAAAGCGC GCCGGTAGAA CGTGCAGGAGC ATCCATCATC AAAAGGGTAA AA	532

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

TTCAGATCAG AAGCAAGGAC AACAGGAAAA GCGTAGGCAC TGTGTTCCAA TTGCTCACAC	60
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1044

CGGTGAAGCG TACCGTGACG CGTACGCCAA AGCGCAGAGG AGTATCGGTC GTAGATTGCG	120
CGCCTGAGGG CAATATTTT TTCTTGCTGC TTTACTTGGA CACACGCGAG CGCCGCGTTT	180
CATATCCGGC ACCATATCAA CGGCAAGCGC TTCTGGCACA AGCGCTGAA GCCGACGCGC	240
GCAAnGCAGCC TCAAAGGCCA TGAGTACCGC GCCGCCGCCT GCGGTAAGCA TATCGTGTGC	300
CTCCAATCCC ACGATGACAC ACGAGCCAAA GTTCCCCAnCT TCTTTCTCC CAATACTGCA	360
CCGACACTCT GGAGAGCTGT CTTCGATGAC GGGTATCCCC AGTTCCAAAA ACACCGCTGC	420
AAGAnGCACA TTTTCCAAGT GTTTCAGGCA CAAGAAGCGC ACGAGCGCCA AGCGCGAATG	480
CCATTTCCAC CACATCACGG GACAACAAAC CGCTGTGATG TCTAAGTCAA GGACAAAn	537

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

TTTAAnTTAnG GATCCCCCTTC CGTTTCCGTC GCTGCCGTCG CCGAGGCCTG TGCACTCCCC	60
GGCCACCGAT TGGAGGCAAC CAAAAACGCT ACGGATAAAA CGCGCATGnT GACCTGCTTC	120
ACACGCGCCC GACTGCGCTG CCCCCGCTTC ACGTTCCCTTG AGCCTGACTC GTTCGCCTGG	180
GACACACCGC CTGGGCATGC CCGACTGTGT TCCCACCTGC ATAGCGCTGG ACTCTCGTTT	240
CCTCTCGTCG TAAAACCGAC AGACAACATG GGAGCCCCGCG GCTGCACGCT CGCGCAATGC	300
AAGGATAACCC TCATAAAATGC CTGCGCCGTG GCGGCCAGTT CTCTCGCAGC GGCCGGGTGA	360
TTATCGAGGA ATTTATTGTC GGAAGAGAGT TTTCCCTGGA AGGGCTnCAT ATTGACGGG	420
ACGTTGTACG TCACCGCACT TGCCGATCGC CACATCTGCT TTCCCTCCCTC ATTCTGTAGAA	480
ATGGGACACA CGCTCCCCGG CAnGCGCTCT GTACACAAAGA CGnACAAGCG CTCATTGAC	540
ACCTTCCACA ACGGTGTGCG GGCA	564

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

CAACTTTATC TTCTATCTTG CCACTCCCCC TAGCCTGTAC GAAACTATCC CCACGCAGCT	60
TGCTATGCAC CACTTGAACC GGGAACAGGG TAATTTTCGC AGGGTAGTTA TTGAAAAAACC	120
CTTGGCTAC AACCTAGAAA CCGGCCAnAC CTTAATGCGA GCTTGCCTGC CCACCTTCAG	180
GAAAACCAAA CCTATCGCAT CGATCACTAT CTGGGTAAGG AAACGGTCCA AAACATCCTG	240
GTCACTCGCT TTGCCAATCC CCTTTTCGAG CCCACATGGA ACCGGACCCA TATCGATTAC	300
GTTGAAATTA CTGCAAGCGA ATCACTAGGT GTCGAAAACC GCGGCGGTTA CTACGACCAG	360
TCCGGTGCAT TGCAGCATAT GATCCAAAAC CACTTGTAC TCCTCTGGT ATATCGCGAT	420
GGAGGCGCCC GCCGTCGTGA GTTCAAGTCG TCTACGGATG AAATCGTAAA AGTCTTGACT	480
GCCTGCGCCC TATGGGGAGA ACGCGACGTC ATGCAGCATA CGGTGCCTGC CCAATACGTC	540
GGGGCAAGA TACG	554

(2) INFORMATION FOR SEQ ID NO: 562:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

ACATTGTAGG TGTCAAGATA CAGACACACG GCGCTGACTC CCATTAGAAA GGCAACGCCAT	60
GCAGACGCAC GCAGTTCTGT ATAGCCTGAC GTATCTGCTG CCCCCGATTC AACGCATCCG	120
TCTTCTTCTT CACTTCTTCG GTTATGTGTT GCTGGACACT CGCGAAAAC GCCGTTATTT	180
CCGTTCGCAT CATCGGCACT AAATCTGCCA GATCCTGTTT CACCTCATCT TGCACGCTCA	240
CCATGGTCAG AATGCTGTT TGCTTACGTG ATAGTTGCTG CTTAATGAGC GCTTCGCCTA	300
CCATTCTCGC AGTATCGCCT AGACTACCCC CGACCGCTTG CATGTTGCA TTATTTTTTG	360
CCACAGCCGC TTGCACTTTC TGATTAATTT CAGTGACGAT TTGCGCTCTGT ACCTGCTCAA	420
ACCCCTTCAC CACCTGCTCC GCATCGTACT GCAGCAAAAC CTGCCCATC AGGGAAAATG	480
CAGGAAGTGC AGGAAGCGGC GGCAGGTTCG GCGGACTTCC CTGCGGGGTG TGAAGATTTT	540
GCACAACCTT ACCGGTAGGT TTAGCAGGAT TAGGCTGAAC TGCCTCTAGC GCGTTTATGT	600
ACGTatCCCC CGAGATTCCA GCGCGCTTCG AACTCCAGCC GTTACTGTCT GCGTCGCCTG	660
TTGCACTACC TGGGTTACCC AGGCTTCCTG TTTTTGACTT TCTCCCTGGA AGAGGTTATT	720

1046

TGAGAGGGCG GTGAGTTAC TCTGCCCT CTGTGTGCGA TTTTGAAAGT CCTGTGCACT	780
CTGGTGTGG TTACCGGC GT CGAGGGCGAA GaGAAGCGGA AGCCGGCGCC TGTTTCGAGG	840
GTGAGTCGGC CCCCTACATT CCACAGCAGT TTATCCTTT CTGATTGTT GCGTCCTTCT	900
GTGCACCGAT GAGGTATCCG TCTTCTAGCG TAACATTGCT GGCAAGCTCT ACCGTGCACA	960
GAGGGTGTCC TG	972

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

CAGGATGGAG AGGGGGCACG CCGCTTGGT GCAAAGGGC ACGATTGTGT TATACCGCTG	60
CCTCCGGGTT GTCTTTAAG GGATGCGCAG ACTCATGAGG TTTGACGA TTTGGTCAT	120
GCCCCATGAAG GTTGCCTGAC GCTCCTTCG GGTGGAAGGG GTGGTGGGG GAATTATCAT	180
TTCCGTGGCC CAGTGCAGCA GGCTCCGCAA CGCGCGCATT CTGGGCAGCC GGGGCAGGAA	240
CGTGTGGTGC ACGTGAACG GCGTATTGTG GCAGACGTTG GCTTTGTGGG GCTCCCCAAC	300
GCGGGCAAAT CTTCTTGCT GAATTTTTT ACCCACGCGC GGTCGCGnTn TGGCCCCTTA	360
TCCCTTCACT ACCCGGATTC CTTACTTGGG GGTGCTGCGT ACGGGGGAGG GCGCGACGTG	420
ATCCTGGGCA GATGTTCCCT GGGnTTCTCG AACGCGCCTC GCAGGGTGTC GGCTTTGGGG	480
TGCGCTTTCT CAAGCACTTG ACCCTGCTGT GCGGGGCTTG CATTCTCAT TGATCTTGCA	540
GATGAGCGTG CGCTGCATAC ATACGAATTG CTTTGCAAGG AATTGTACGC TTTCTCCCCT	600
GTCTTGAGA nAAAAGCGC	619

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

GACAGACATT ATGGAGGTAA TTTTGTTTC ACTTGCTGGA GTTTCCGAAG GAGTAGAAGG	60
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1047

ATACACAGTG CATGGGTCAA TGGTGCAGCG AATGTAAAAA CCTCGTGTG ATTTTCAGAT	120
GAAAAGCGTC GGTACTCATG AGATTTTATG TTCAGGAACG GTTCCTCTTG AATATTTAA	180
CGAATGTTA GGTACGCCGT TGCACTCGCG CGTGTACCAC ACGGTGGGAG GTTTACTCCT	240
GGAACGTTT GGACGTCTCC CTACGGTAGG GGATGAGTTG GTAATTGAAG GATTGCGTTT	300
TAAGATAACGC CGTGTACTCG ATCGGTATGT TGTGTCTGCC CTCGTGGACA CTCGAGCATG	360
TAGTCAAGCG TTGGCTGACG CCTAAGTAAG TACACAGGAT GGGGGCCGTA CTTTGCGGnA	420
TCTGCAATTAGTTGATGT TGGATCGTGT TCTACAGGAA TGTGTGCGCA AAGGGTGAnA	480
GCAGAGTTGC TACnTGTGA AGTGGTTCC CGTTTCAGGT GTATCGCGGT GTGGAAA	537

(2) INFORMATION FOR SEQ ID NO: 565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

CACGTTCGTA ACAATTGGAC TGGTAGTGCA TGAGCGCTTC CTCACCTTTA AAAGTACTGG	60
ACTATTTACG GCACCACAGG ATAGAGGGC ATTGTAATGG GAAGGTGCTG CTCTGTGCAA	120
TGCTCACAAA AAGTGCATGT CTTGAAAAAG TGTACCAGAG CCACTACACT GGTGCCGCG	180
GGTCTGCTG TTTCTCCGAA AGTTTAAAAA GGCTTTCGCG ATCTTTTACC GGATGAAGAG	240
ATTGAGCGTG CATTGCTCGT AGAAAAACTG ACGGTGGCTT TAAGACAAAT GGGTTTTGTA	300
CCTATCGATA CCCCCCGCGTT GGAGTACACC GAGGTTTGTC TGCGCAAAAG TGAGGGTGAC	360
ACAGAGAAGC AGATGTTTCG CTTGTTGATA AGGTGGAAGA GATGTGGCCC TCCGCTTTGA	420
TCTTACGGTG CCGCTTGCGC GTTCGTTGCA ACGCACTATG CGCGTTGTA TTTCCCTTTAA	480
GGCCTATC	488

(2) INFORMATION FOR SEQ ID NO: 566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

1048

CCTTTGCCCT	nTTGTTGGA	ACCCATTCC	CAAGGCCGGG	GAAACTTTn	GGGGCCCGTT	60
TAACCCAGGG	GGAACCAACC	TTGGAACCCA	ATTCCCAGGC	CCCnGGAATT	nGCCCAACC	120
GGCCGGCTT	TnCAAAACCG	TTnCCAGGCC	GGCCGnATTC	CAGGGTTTTG	CCTTGAGGT	180
TCTTAATCCC	CTTTGGATTA	TTTTAAAGGT	CGGATTACTT	TCCAAAGGAC	CAGGAAAGAA	240
ACTTTGCCG	CTTCTTTGGA	AAAGCCGGTT	GAGCAAATT	TTTGCACCGC	CATGCTCGTC	300
AGGAGCGGGG	ATGTACTCAG	GAGTTTGTA	GCCCCAGTAC	TATGCCACCT	ACCGGCACGT	360
AGGCCTACCT	GCGCTCGAAC	CGATCTATGC	CGTACGGCG	GAGCTTGAGT	CTACTCTGCA	420
GGATTTACGC	GCCAAGCGTG	ACCAGCTCTT	GGAAACATGC	ACATTGGTT	CAATTCTTGA	480
AAGAGTTGGC	CTCCAGGCGA	AGAGCGGGT	TGTTCAGCGC	AGGATTCGCG	TGCTCGAAGC	540
AAAAATTCAA	AAGATTATTA	CGCTCTGTAC	CCCGGATGTC	ATTGCGCATC	CGGACGTCGA	600
GCGCATGTAT	CACGCAGGCG	AGCTTTCTC	CGCACTCAGT	GCCGCGTACG	CACGGCTCAT	660
ATCCGACCGC	GGCGTTACG	CGAGCAACCT	TCAACATAGC	CAGGAGCTTA	TGGATGAGCA	720
AGAAGCACTC	GACGCGGCC	TGCGCCCTTG	ACTGTGGTGC	CAAGCCGCTG	AAGCGCGTTG	780
CGCGTTCAC	AGCGCAGGTC	AGTGAACCTGG	ATGAGGATAT	CAATGCGCTG	TGGGCGCATC	840
GGTGCTGCAT	ACGCAAGTTG	TTTCTTTACC	GAGGAAGGAT	TTGnTCAGCC	TCCTTTaTCT	900
CAGAAGACAA	GACCGACGGT	GCCCCATGAA	CTCAGCACCG	TGTTGCGTAC	CGTGGCAGAA	960
GCGCGGATGC	gTAGGGCACG	TGCAGGGTAT	CAGGTAGAGT	GCGCCAAGCT	CCGTAAAAG	1020
CTTCAGTCAG	AGCAGCGTGT	GTGCGAAst	TTTGCAGATC	AATCGaGGAA	TATCGACGGG	1080
GGATcAAAGA	GTACGAGGCG	ATGATCGAAT	CGGCGCACAG	AACGTGCGT	TAAGCAAAGC	1140
CACGGTAGCG	CGTCTGGCGC	AGTCATTAGA	GGAGGGTCA	GAACGCCCTTA	CCCTATTGCA	1200
AAACATCGCCG	GAACCTATTG	TTCTCTCTTC	GGAAAGTTCTG	TCTGTCCCCC	AAGAGAAGGC	1260
GAGTGTGTAG	GTGCTCATGA	GATAGAGCTC	TCCGTGTCTT	CTAGACGGGn	GGGGGGGGGG	1320
TGAGGTAGAA	GTGAGAGGAG	GGGGAGTGAG	TGGGCAGGCA	GGTGATGCAA	GCGGGGGTAC	1380
TTGCGGGCAT	GGTATGTGCT	GCTTCTGGTT	ATGCAGGGT	ACTCACTCCG	CAGTCAGTGG	1440
CACAGCCCAG	CTCCAGTGGG	GCATGCGTT	CCAGAAGAAT	CCACGCACTG	GCCCCGGCAA	1500
GCACACCCAT	GGGTTTCGCA	CTACCAATAG	TCTGACTATT	T		1541

(2) INFORMATION FOR SEQ ID NO: 567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1049

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

CTGTGCTGCG CACCGTGCCA GCTGAGCGTC ATACCCGGAT CATTAGA GAACTGCTTC	60
TAGGACTGGT GCTCATGCTC TCCTTCCTTT TTTGCGGAAA AGTTTCCTA TCTTTGTTCC	120
AGCTAGAAC GGGAGTAATG AAAATGGCCG GAAGCGTCAT TCTCTTCCTC GTTGGCATCA	180
AGATGGTATT TCCTGATCAA CACGCGCTCC CCTCCACCAC AGAAGAGGAA CCCTTTATTG	240
TTCCCATCGC CACTCCCAGT ATCGChGTCC TTCGGCGTTC ACCACCGCTGG TAATTATGGG	300
AGAGACGAnG GGACATCCCG TCTGCCACC TGTGCTGCGC TGCTTGTTGC GTGGACGCTC	360
GCGTGTCTTA TTATGATAAG CGCACCGTGT CTATACCGTC TTCTTAAAGA AAAGGGAATT	420
ACCGCGCTGA GCGAATCACn GTATnTGCTG CTCATTCTTC CATCCAGA	468

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

CCTGACATGG TGCACGGATC TGGAAAGAGGC GCTCTATCAT TGTGGGGCGC TTACTGGAGA	60
ATGCACAGCG AAGATATCCT AGATGCGCTG TTTGAGAAGC TCTGTGTGGG AAAGTGACCT	120
GCAGTACGGG AGATAACGGGC GCGTGTGACT GATTAGTTAT ATTTCTTGGG GATGCAGCGT	180
CAGGTAACCTT TTTTCGGTAG AAAGGTGGAG GCGCGCGCCG TnCTGAGTCT ATGTGCACGC	240
ACGATCCTGC GCGAACGTT CCGTGAATCA TGCGCACGCA AGCTCATTTC CAATTCTTG	300
CTGCAATACG CGGCGCAGGG GCGTGCAGCC AAGAATGGGT CAAAGCCGTG TTCAAGACAG	360
TAGGCCTTTG CAGCCGCGCT GTAGCCAGCA CAATATCTTA CCGCGTAAGG TTCTGCGAGC	420
TCTCATTCGC ATCTAAAATT CCTGCAGGTC TCTCGCTCAA nGGAGCAAAC ATACGCATCG	480
TCAAAGCGAT TGAGAAACTC CGAGAGA	507

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1050

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

TGCACAAAnGA	TGCGCGGTAA	CACCGCATGC	GATTGAGCAG	GTGTGGAACG	ACACATCACC	60
GTGCAGTACG	CCTTTGGnTT	GGTACAGGAT	GCAACGCATG	TGTTTTTTTT	GTACGCGCAT	120
GAGCCCATGC	GnGATCCGGC	TTTTATTTTC	TTTTCTGGAG	TTGCTTGTGG	GCGTGGTATG	180
CACGTGCTGC	TCTTGGCTAC	AACAACGGAG	GTCAGGGATA	TCCATGTATT	TCGCGACTTG	240
GTCTTTTAC	TTGAGGACGA	GACGTTGAG	GATTTCTTTC	GTGTCGAGCA	CGAGAGATTT	300
GTAAGGCAGA	AAAAGAACG	TGTCGCACGC	ACTGCGCTGT	TAGAGCGCGG	TTATCCATGT	360
TTTGAAGAAA	ATTCATCGCG	ACATCATGGA	TGGGAATATT	GATATGTCAA	CTCTTTGGAA	420
GCAGGATTAG	CGCTGCTTGA	AAGACGCACG	CGGTACCCCTG	TGTTGTCTTG	GCAGTGCAGGG	480
AGGTCAAGGAT	GAGAGGCAGC	GC				502

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

GACGAATGCG	ATGCCGACGG	GTGATGTAAA	TGCGATAAAAG	CCGGCTTATC	TTAACAGTT	60
GCAGGATATT	GGCTGGAAAC	TGGAGGATCA	CAGCCGAGAG	ATTCGGGAGG	TTCGCTTAC	120
TATCGAGGCG	GGCAGTTTAT	GGCTTATTGA	GCAAAAACCT	GTCGAAGCGA	AGAGCACAAAT	180
CTCTTTGGTA	CGGTTGCTGC	TCGACCTGTA	CGAGCGCGAG	GTGGTGGATG	CTGAATACGT	240
GGTCAAGTCG	GTAAAACCGG	GTCAGCTGAA	CGAGATTTG	CACCCGGTCA	TTGATATGAC	300
GAGTGTGACA	GGTTTGAAAT	CCTCCGAGGG	GGGATTATTG	GTGTTCTGG	TGCGGCGGTT	360
GGGCGAGTGT	ACTTTACCGn	CTGATTCCCT	CATGCGAGGA	CGTGGACGTG	TGGACGAAGA	420
TGGGCGGACA	AGATACACGG	TGTATCTTGT	GnTATGCCTG	CAACGnACGC	GGGGGAnGTT	480
AAGGGCAATT	GAGGTGGCAA	CTGGTGTCT	TTCTAACGAG	GGGGGGTACT		530

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs

1051

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

nTCTTTTnG	CATA CGGGGC	ACGGGGACTC	TGTGTGCCAT	GTCCGTTTTT	TGTCTACTTC	60
TTTCCTTG	AAGGC GCGTGT	GTGGCGGCGG	ATAATTTCCT	TTCTTCCCTT	GTGTGGAATC	120
TGGTTCTTGC	CTTCATCCCC	TGGCTCATCT	CGGCTATCTT	GCACGTGCnC	nGGGGGGGGG	180
TCCGGGGGGG	GGGGnGTTCC	TTATGCTGCT	CTGGCTATTG	TTTTTCCCA	ACGCTCCGTA	240
CATCCTTACC	GATATTATCC	ACTTGGAAA	GGGTAAGTCA	TTTTTGCTTT	ACTATGACCT	300
TATTATTTA	CTCGCCTATA	GTTC ACTG	TTTGTCTAC	GCGTTGTCA	GCCTTCACCT	360
TATTGAAAGC	ATATTAGCCC	GTGATTTCA	TATCAAAGG	CCATCATAAT	TTCAGTATTT	420
GAATTGTATC	TCTGTGCATC	GGTATATATC	TGGGGCGTTTC	TGCGCTGGAA	TTCCGGGACA	480
TGTCCTACAG	GACGC ACTAA	TCTTCTGAA	TnTGGTATCC	G		521

(2) INFORMATION FOR SEQ ID NO: 572:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

AGAAAGTGGTC	CTGCAACTTT	ATCCGCCTCC	ATCCAGTCTA	TTAATTGTTG	CCGGGAAGCT	60
AGAGTAAGCT	TGCTGCACAC	GAGGGCGCA	AGGC GGCGTG	CGCACCGCCT	ATTCCCTGGG	120
AGCAGCTCAT	GTGCCAGATG	CGTGCACAAT	CCCGCGCGCA	CACCGTCGGC	GAGCTTTCT	180
CTCCGTGGAA	ATCGTAATGT	TCATTGTT	CGAGAGAAAT	AACAACCCCG	CAGTCTATGA	240
GGGGGTGCCG	TACTCAGCAG	GATTGGTA	TATGTGCTCA	AGCGCGATCT	GTGTTGTGC	300
AAACAGCATG	ATACTTCTG	TCGCAGTCTG	ATAACGCTTC	TCAGCAACGA	CACGCACAAT	360
GCCGCAGTTA	ATGATGAGCA	TTGCACAGGT	GC GGACGGT	GTCATGGTAC	AGTAGAGTGT	420
TGCGCCCTCT	AGACCGATGC	CCAAACGCGC	TGCCTGGCAA	GGGCGTTTTG	CTCTGCGTGC	480
ACGGTGCGAA	CGCAATGCTG	CGTGCACGTC	CCGTCTTCAT			520

(2) INFORMATION FOR SEQ ID NO: 573:

1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GC GG GT TT AT	TAG AG TT GAT	TGT GC AGG AA	ACG CATA CGA	TTC AT ATT AG	AAT TT CG AGT	60
TT GT AC CC AG	AA AG CG TA AC	AT CT GCT TTT	TT GCG TG CT A	TT GCG CAC AC	GCG CGT GT CG	120
CCT CATT TT TC	AT TT AT CG GT	TC AG TC GGG C	AG TG AT CG CG	TG TT AC GAC G	CAT GCG AC CC	180
GCT TAC AC AC	GT GCG GAC AT	TT AT CAGG CA	GT TT CCG ATT	TAC GG AGT GT	GCG TGA AG AA	240
CC CTT TT GGG	TT GT GAC ATA	AT CG TC GG CT	TT CC AG GG GA	AA CA GAG GAA	GAT TTT GCA G	300
AC ACC CAG CG	TAT GT GCA AA	ACT TT GCG TT	TT GCG AGG TAT	CAG TATT CCG	TTT CT GCA CG	360
CCCC GGT ACA	GAAG CGT TGC	TAT GG AT GCh	AA AT GC CT CA	GCG TATT GCA	GG AGA AC GCG	420
TG CT GC AT GC	ACA ACT GG CA	GAG AAA AACT	AAC GT GCG GT	ATT GGA AT AT	GG GA AG GG AG	480
GA ACT AGT GC	GG TGG TAn AA	CAT CCG TCG C	AC GT Gn TTT G	AC AG AAA ATT	AAT	533

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

TC AT TAGG CA	CCCC AGG CTT	TAC ACT TT AT	GCT TCC GG CT	CGT AT GT TGT	GT GG AAT TGT	60
GAG CGG AT AA	CA AT TT CACA	CAGG CA AT AT	TCCC AT CT TT	CGT AC AT GC	GCA GT AAA AAA	120
AG AGA AAC AGA	GT CCC GTT CC	TTT ACC CAC G	CT AT CA ACT C	AT TT GCG CAA	TAT TT CAG CT	180
GAT T GAT AGT	CAT AGG AAT G	GC AC CT GCT T	CG GGG GAAA	AA CT GT CT GA	AT CG AAT CAA	240
CA AT AA CG AA	GG TAG GG CAT	CGT GT AT TT A	AA AC AC GCT C	GAC AT CCT CG	ACCC CG GT CG	300
CAC AA AG CAA	CT CG AT GT TC	TGA AT TG GAA	TAT TCAG CCG	AT CC GCA CG C	CC AC GA AT TT	360
GCC CCG GAG A	TT CT TCAC CC	GAA AC AT AGA	GAAC CG AT TT	CCC GCA GCT G	CAG CG AT TT G	420
TAAC AG TAAT	GT AG AT TT AC	CA AT GCG CCG	TT CCCC GCCA	AT CAT GAT CG	CGG AGT CT TT	480
ACGG CGC CTC	CGCC GAGG AC	ACG AT CGA AC	TCT GCG AT AC	CAC AACT AAT	ACG CT GCG CA	540

1053

562

TCC TGC GCG GC ACAG CACA CA

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

GTGCAACTTT ATCCGCCCTCC ATCCAGTCTA TTAATTAAAT CTATCGTTGA AGAGGTATCT	60
GTACCGTGAG CCTCTGTGCA AAAGCCGTAG TTGCGCGCGT GTGTGACTCC TGCCTAAATG	120
TTCGCACAGA AGAAAGCGTG TCGGTAACGT ACATGCGAAT GATGTCTGCA GCCTTTCCA	180
TCTCTTCTC TCGGTAGAGC AGCCATTGTG CATAATGCGT GTGCTTCTG GAGAAATGAA	240
CGGACTCAAA GCGGTTGAGA GAAATAGAAC GCACAATCTT TTCGCAAAC CGGATCAGCG	300
TGCGCACGTC GGTCAGGTG AGGGGCGCAA CC CGCGCGGC GAAAAAAATCA ATAATTTCT	360
TTATTTCTTG GATTTCTTC TGAGCGAGCT CTGCTAGGGC ATCGGCAAGC ACTTCCTTAA	420
ACCGCACGTC CCTTTGCGA TAATAGGACA TGAGGAGTAC CCTACGCTCC TTCTGAG	477

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

TTCTTTAGCA CCTCCAGCGC TTAGCCTGAA AATATGAAAC AGGTCTGTGC ACCGCACCAC	60
TTGCGAGAGT CCTGGGTGAG AGTGAGGAGC AGGGnCCCGn AGGGGGGGGG AGGAGGACAG	120
ACCAGCCTGA GCAGCACTGC CTGAGAAC CCACAGGCTG CAGCAAGGC CAATACAAGG	180
TTTACTCAGG GCCACATCTG AGCAGCCCAG GGCCAGGCTC CCCAGATGGC CACAGCGGCC	240
AGGCC TGGnC CAGGCCAAAG CCAGGAGCCA GGAGCTGCAT CTGGTCTCC CACGTGGTG	300
ACAGGGGCC ATAGACTTAG GCCATCTTCC CCTACTTTCC AAGGTGCATT AGCAGGGAGC	360
TGGATCAGAA GTGGAGCAGC CAGGACTCGA ACTGGCGCCC ATATGGATG CCGGCACTGC	420
AGGGTGCCCT GGAGAGCTGC ATCTGAaCGC CCTCACACAG GGCTCCGCAG GGGTTTCTCT	480

1054

CGAATGCTTT GCCGGGTTTA TGGGGATGTG TTTGTTCTCA CTGCCAGTnG GAnCCTGAGA 540
 TCCCCGGCCT GCTGTGCAGG AGCTCCTGC 569

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

TGTTTTCTCA GGTTTCTAAA GCTTCTTCCT AGAAAACTCG AATGTGTGGA GGATTTGACT 60
 CCAGGTGGAA CCAATTAGCG TTTGGCAGCT AAAAACAAAA ACTTACATGC TAAAATGCAT 120
 TCAAAACCGT AAAGTCCATA GAGAATGTCC AGAAAACACA AACACAGAGG CAGTAGCAAG 180
 ATCTGGGATT GAGATAGCCA CAACACACCA GATAGTTTG TTTTCATTAA GGAGTATCTG 240
 GACAAATTGT TGTAGTTTG AAGTGAATT TAACCAAAAA ATCACCGTGA AAGTGGTTTT 300
 GGAGAAAAGC ACAATCTTGC TGTCAGCAA ATGCATCCAA TGTCACTTTT CCAAATACAA 360
 ATATCATGTT TTCTCAGGTT TCTGGAGCTT TCTTCCTGGA AAACTCGAAT GTGTGGATTA 420
 TTTGACTCCA GGTGGAACGA ATTAGCGTTT GGCAGCTAAA AACAAAAACT TACAGCTAAA 480
 ATGCATTCAA AACCGTAAAG TCCATAGAGA ATGTCCAGAA AACACAAACA AACACAGAGG 540
 CTGTAGCAAG ATCTGGGAT GAGATAGCCA CAACACACCA GATAGTTTG TTTTCATCCA 600
 GG 602

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

GTGTTTTCTG GACATTCTCT ATGGACTTTA CGGTTTGAA TGCACTTAG CATGTAAGTT 60
 TTTGTATTCA GCTGGCAAAC GCCAATTGGT TCCACCTGGA GTCAAATCCT CCACACATTG 120
 GTGTTTTCTA GAAAGAACGCT TTAGAACCT GAGAAAACAT GATATTCTT TCTGTAAACA 180
 TGACATTGGA TGCATTGCT GAACAGGAAG ATTGTGCTTT TCCCCAAAAT CACTTTCACT 240

1055

GTGATTTTTT GGGTTAATTT TACTTCAAAA CTACAACAAAT TTGTCCAGAT ACTCCTGGAT	300
GAAAACAAAA CTATCTGGTG TGTTGTGGTT ACCTCATTCC CAGATCTTGC TACAGCCTCT	360
GTGTTTGTGT TTTCTGGACA TTCTCTATGG ACTTTACGGT TTTGAATGCA TTTTAGCTGT	420
AAGTTTTGT TTTTAGCTGC CAAACGCTAA TTCGTTCCAC CTGGAGTCAA ATAATCCACA	480
CATTCAAGTT TTCTAGAAAG AAAGCTCCAG AAACCTGAGA AAACATGATA TTTGTnTTTG	540
GAAACATGAC ATTGGGATGC ATTTGCTGAA CAGCAAGATT GTGCTTn	587

(2) INFORMATION FOR SEQ ID NO: 579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

CGCGCTTGCA GTTCAGGCTC AGTTTGCGCT GATTTCTCT ATCACACCAG ACATAAAGGC	60
CCAAGAAGAA GTGATCAGCC AGTCGATGGT AGAACAGACG AAAGACAGTG TGCACGTGTT	120
GCACGCTATA CAGCACATCA CCGAGATCAC GCGCACGTTG CAGGAAAATT CGGGCGCCAT	180
CTTGGACAAC AGCAAGCACG TAGAGGAGgG CGATGCTAGC CCTTCGCGC ATCACGTCTG	240
AAATCGACAG CAGCGTGTG TCCATGCACA AAAACTCAGA ACAGGTTAAA AAGTATGCTT	300
CCTCAATCAC TGAAATCGGA CAGAAGAACAA AGGATTCCAT AACGGACCTA GTCACTGAAT	360
TGAGTAACAT GCGACTCTAG AGTCGCGGGG GCGCCTGTTA CCCTTCAGCT GCCATGCGTC	420
TGCGCACTTC GTGcaGGTTA GGC GTGTGTC CTTTCGCGTA GAAAGGTCGC GCA TACGAGC	480
AGGCAGTCCT CCACCACGGC GTTGCCTGT TCAACAAAGA TCCCCCACCT AATCCCCTTC	540
TTCTCTGCAA AGGCGTACTG TTGGCTCAAc TTCCGCGGAT CAGGGAAAGAC TTCCGTCGCC	600
ACCTGCACTG CAAAGTATGA ACACAGCTTT TGGTACACAT CCATGAGCGC ACTAnCCTGA	660
CAGAAAGATA AGCGCCTGCA CAAAACAAAC GTGCTCTCGG GAC	703

(2) INFORMATION FOR SEQ ID NO: 580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

AGTCAnTTCA ACGTGTTCGG CCGTGGCATA CAGCTCCCTG GTCTTCCTGA TTATCGCCCT	60
CGTGGCAGG TTTCGCACAG GCCGGAGAAG ACAGGCTCCG CGGTACGCAC GATAGGCAGTT	120
TTGATAAGTG CGCGCAGTGC ACCACCGCCT GAAACGACAA TGAGCTTCCG TGAGCGTCTT	180
CGTATAGGTA CCGTTGAACG GAACGAACGA ACCGCCCCGAG AAGCTCTATG TCGGGCGTCT	240
CAGGCGAAC GATGGAACCT CCAAGTGACA GAACGGTGAC CATGAAACCC TCTCGCCGGC	300
ATCGTAACGC AAAGAGACCC TTTGGATCCA GGCCCTGTGT GTATCTGGCA TTGCGTCCCA	360
GCGTGCACGG GGCGATGGAG TGTTCTACAC GGGCGACACA GACTCCTAGT TCTTGTATTG	420
TGTGCAAAAA CCG	433

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

GATACGCAGC TTGCGACGGT GAGCTACCGC ACGTACACCG TACCTAAGGG AnCATACTAT	60
TAGTGCCATT GCGCTGCGCC AGGTACTCAA GCATATGGGG ACGCTGCTGT CGGTGAACGG	120
AATTTCAAAC GCGCGCAGAC TATCGGTAGG GGATCAAATT ACTATTCCGT CCATGGATGG	180
ACTCATGCAC ACGGTACAAA AGGGGCAGTC GCTTAnTGCA ATTGCCAGTC TCTTTCGTTT	240
GCCCCTGAAT ACGTTGCTGG ATGCGAATGA TTTAGTCAnT CGTGCATTAA CAAnTTGGACA	300
GCGnTTGTTT ATTCCGGGTG CAAAATTATC TGCTTCnGAT TTnAnGAAGG TGTGTTGGGGA	360
GTTATTTCATG TATCCAATTC GCGGGCGGCG CACCTCTGGG TTTnGGTACC GCTCAGATCC	420
CTTTTCAGGC AAnAGGAGCT TTCACAATGG GA	452

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

1057

CGCGATCCGC ACGGnCAnGG GGCAGAAGCC TGCACGGTG GTGTCGGTGC GCGATTGCTC	60
GGTGGTGACT TCTGGTGCCT ACGAGCGTTT CTTTGAGCGT GACGGGGTAC GCTACCATCA	120
TATCATCGAT CCGGTTACCG GGTTTCCGGC ACACACTGAT GTGGATTCTG TGTCTATCTT	180
TnCACCCCCGT TCCACAGATG CAGATGCGCT TGCTACCGCC TGTTTTGTAT TGGGGTATGA	240
GAAAAGCTGT GCGCTCTTGC GTGAATTTC CGGTGTTGAC GCGCTGTTA TTTTCCTGA	300
CAAGCGCGTG CGCGCAAGTG CAGGGATTGT CGATCGCGTG CGTGTGCTCG ATGCACGTTT	360
CGTGTAGAG CGTTAGGACA GCACGTGTGC TGTTCGTGTG TAAAAAAATGT GGC GGATGTC	420
CTCATCAGGT GT	432

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

CTGTGCTTAT CAGCACGCCA ACTAAAAGTC CAACGATGAC GCACGTACGA CACTTGACTT	60
CTCGTGCCTA GTGAAAAGA AGCGCGCCGT ACATGCATGG CAGCGCGGT AAAATCCAGC	120
GTAACGGCAC TCCCCACACA GCTTCTTCTT TGCGAAAAAC TGCGACGATA TTCGGTCCAG	180
ACGAAAAAAA GCAAGCGCTG AGCACTGCCA CCGTACAGAT CGCAGAGAGG AAGGAAAGAA	240
CGCGGTGCAT CGGTCTGTCC ACGTCGCACG AGAACAGGGT GACACTCAAG TGTTTACGTT	300
CACGCGCAGT AAAATGCCTG CAACACAGGA AAACACGAAG CTAACGTGC AACCGCGGCG	360
TTCAnAnGAG GAGAAAAAAA GGAAATGAAT CTnCGTGCAC GGAGAAAACC TCGGAACCTA	420
CGCCCCGCTA AGAAA	435

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

TGCAACACAC CCCGAGCACG CTCGGCGTTG AGCTTACTTG AGAGCGnnGG CGTTGCACCC	60
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1058

AGAAAAGGAC AGAAGGAGCA GCAGGCTGCG TGGACGCACC GCGCACGCCGC GCATCCCGCT	120
GTGCAACAAG CGGAGCACCG GTACGAGTAG CGGGAGGCAGA CTTGGCAGAC GCTCGGTAC	180
TCCGTGCATG CTTTGACCCA CCCTTGTACT CTGCAGATTG CCGAGTGTCA GAGGCAGGAG	240
AAGTTTCCT GTCCTGCGCC GCGTCTGTGC GCTCAGCAGC CGCCGGAGGA GAAACATCAA	300
GAnTTTCGCG ACGAGCGGTA GGGACnTCCT TTACCACCGT GAGnTCAGGA nTGCCCTCT	360
GTGTTGGCGC AGGACTnTTC CCCAGCTCAG GAnTTTTTC AGGnTTTTTA GCCATAAGCT	420
CGGnTCCATG ACGG	434

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

TCTCTCATAC TGCTCnTACT CCTCTCTCAT CATTGTCTCT CCCCGCTGTA CATCCGCGCG	60
GTGnCCGCAC TGCCAGACAC CCTTCCTCCT GTGAGGCTGG TAATCGGCGT TGGAATAAAA	120
GGGCAGGGTA TCGCCTGCTT GCATTCTGCC GCCCTTCCTG AGAAGAAGGC GCGCATCGGC	180
AGTTCACTGA CTACCCCTTCC GGCAGCCTCC GGTGCATCGT GCCTCACCTT TTTTACCGT	240
GGACACATAC CCCAATTCGCG CATTCAAAA AGTCCGTTGA ACAATCGTTC GTCGTTTCT	300
TACACGCAGA TGTGCAACAA CTACGAACGC AAAACATCAC GTGGCTTGGAA TCCATTGGC	360
GGACCGACCA CCCCCCTGTC TTCCATTCTT CGATTAGGGCG CGCGGGGAT TGTAGCCTAT	420
CTCAATT	427

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

CGGTAACACG TGGTTTGCAG CGCAGGCATT GGAGTAATTG ATCGTACAGG AAATCCGGTT	60
TTGCCCAAT TTTTCAATG AGCGGAGAGA TAATCCCGTC TTTCTGGAA AGTAGGGCGT	120

1059

GGAGTAGATG TTCCCTCCTCA ACTTGACCGT GGTTCTCCGC TTCTGCCAGA GATATGGCGT	180
CATTGAGCGC TTGCTTGCT TTGACTGTGT ACCTGTCGT GTTCATGGCG TGATTATAGG	240
TCTTTGAAC GCTTTTTCT CGTCATCGGT ATGTTTTTC TACCGCTTGC AGGGGACTTA	300
CGGGAGTAGT CGCGGTGGAG AACAGGGGTG TACATGGTAT GCGGTGCGCT TTGGCAGGCC	360
GCGTAAGGCG TACCTTnTAT ATTTTCTGTT TTGAATAGGC TCCGCGATTG GGAGTTGGGA	420
ATAGGAAAAA	430

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

GnCCCCATCA GGGAAAATGC AGGAAGTGCA GGAAGCGGCG GCAGGTTCGG CGGACTTCCC	60
TGCGGGGnTG TGAAGATTT GCACAACCTT ACCGGTAGTT TAGCAGGATT AGGCTGAAC	120
GCCTCTAGCG CGTTTATGTA CGTATCCCC GAGATTCCAG CGCGCTTCGA ACTCCAGCCG	180
TTACTGTCTG CGTCGCTGT TGCACTACCT GGGTTACCCA GGCTTCCTGT TTTTGACTTT	240
CTCCCTGGAA AGGTTATTTG AAAAGGGCGG TGAGTTCACT CTGCGCCCTC TGTGTGCGAT	300
TTTGAAAGTC CTGTGCACTC TGGTGTGGT TACCGGCGTC GAAGGGCGAA AGGAGAAAGC	360
GGAAACCGGG CGCCTGGTTT CCGAGGGTGA AGTCGGCCCC CTAACATTCC ACAGCAGTTT	420
AATCTnGGCG nGCGTTGTT	439

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

TTCACCACG AGGTGGAGCG CTCCCTGCGC GTTTTAGACG GTGCCGTCT CGTACTCTGT	60
TCGGTTGCAG GCGTCCAGTC CCAGTCCATC ACTGTCGACC GGCAGCTCCG CCGCTATCAC	120
GTGCCCGTA TCTCATTAT CAATAAGTGT GATCGTACGG GTGCCAACCC TTTCAAGGGA	180

1060	
GnACTTGTGG CGACAGCGCG TGCAGCAACG TGAAAAACAG CGCTCGTAAG CTCCCCTGCG	240
ATCTTATAACA TATTGGGAT CATAAGCAGC AATCCCTGAG AAGCAGTAAA AGTAGAAGAG	300
AGGCCCGCCCG TCGTCAGTGC GCCATGAACA GCTCCCGAAG CGCCTGCCCTC AGACTGAAGT	360
TCTACAAACGG TGGGAACGGT ACCCCAGATA TTTGTGCGCC CCCGTGCGGA ATATTCGTCT	420
GCGATTTCTC CCATAGGACT GGAGGGAGTG ATAGGGAAAGA TAGCAATGAC CTCACTAAC	480
GCGTGAGCAA CGTGCCCCAn TGCGGTGTTA CCATCCATCA TGACGAGGTT CTTCTCAGAC	540
ATACGAnCGT CCTCTCTC	558

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

TAATTCCCGA ACAACnGTGC CAATCGTACT CCGCAATATT CACCGACAGC AACGCTGTCC	60
CCTTCCTTnCC ATTGCTTCTA GTAAGCCCTT AAGCCCAGGG GAGAATCTCG CGCTGGTAAT	120
CGTGCAGGGC TTTTCCCTTA ATTCTCAGGC CATGATCCAA ATCAGCGATG TCCGAGAGAG	180
TAAAGCAGTG ATAAAGACTT TTCAAGAGAG CAGAAAAGTC ACTGACCATA GCGTAnTCTC	240
TGCAAGATTA CCGCTATGCA TGTTTACTGC GATTTCCTGT AACGCAGCTG TGC GTGCAAG	300
GAGAGTGGTA CTAATCTCAC GCAAGAGTGC ACGCACTCTC CCCCTGAAAG AGTGGTAAGA	360
TTAAGGGTGA CGTCGGTATC CAAGGATTGG CA	392

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

CCGATAnCAT TACCTGGGAG GGGGATGCAC GCATTGTGCA GGCAGCGCGT GTTTCTTACG	60
GTGCGGGGAC TAGGACTGCG CGTGACGATG CGGCGCTTAT CGATTTCTT TTACGCAATA	120
AGCATAACGTC TCCTTTGAG CAGGTGGTCC TTACCTTCCA TGTACGTGCA CCGATTTTG	180

1061	
TCGGCGTCA GTGGATGCGG CATCGCACTG CTCGCATCAG TGAGGTGTCT AGTCGTTATT	240
CGCTTCTTAG TCATGACTGT TATGTTCCGC AGAAACTTCA GTTGCAGTTC AGTCCACGCG	300
TAACAAGCAG GGCGCGCGT CCGAAGTATC TCTCCTGAAC AGCAGCAGGA AGTGCAGGCA	360
GCGTTGAAG CTCAGCAGAA AGCGCGGTGT GCnCTTTACG ACGCATTGAT CAAAAGAAC	420
nCGCGCGGGGA GCTAGCGCGT ATTAACGTGC CGCTTTCGCT TACACCGAGT GGTATTGGCA	480
GATTGATTAC ACAATCTTTT CATT	507

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

TCCACCTGGA GTCTATAACGC CACACATTCC GTTTTCTAGG AAGAAGCTTC AGAAAnCcTGA	60
GAArACaTGA TATTTsTwTy TGTAAACATG ACATTGGATG CATTGnCyG AAYAGGAaGA	120
TtGTGCTTTT CTCCmAAACC wCTTCACGG TGATTTTGGA TTAArTtTCA CCCGAAwTCC	180
ACAAsAATTG GTCCAGATAC TCTGGATGAA AACAAAAC TA TCTGGTGTGT TGTGGCTATC	240
TCAATCCCAG ATCTTGCTAC AGCCTCTGTG TkTGTtTGTG TTTTCTGGAC ATTCTCTATG	300
GACTTTAmGG TTTTGAATGC ATTTTAGCAk GtAmnsnTTTT TGTTTTCAGC TGGCAAACGC	360
TAATTGGTTC CACCTGGAGT CwAAATmCkCC ACACATTGGA GTTTCTAGG AAGAAAGCTT	420
CAGAAACCTG AGAAAACATG ATATTCTTT CTGTAAACAT GACATTGGAT GCATTTGCCG	480
AACAGGAAGA TTGTGCTTT CTCCAAAACC wCTTtCACGG TkATTTTGGA TAAATTcAC	540
ycGAAwwCyA CAACAATTGg TCCAGATACT CCTGGATGAA AACAAAAC TA TCTGGTGwkt	600
TGTrGCTATC TCAATCCCAG ATCTTGCTAC AGCCTCTGTG TGTGTtTGTG TTTTCTGGAT	660
ATT	663

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

AAAAAAATAAAC	TGCGTGTCAA	AACCCACACC	CTCAAAACGG	ACCCGGCGAG	CAGCGCCACG	60
CACTGCACTA	CCC GCCTGTC	TTACTGAACA	AAGAACGCC	TTATGCGCGC	GCACCCCTCGG	120
ACCTTCTGAA	CGTCCCTACC	ACTGAGGCC	CTTCCATTCA	AAATCATCCC	ACTCTGCAAC	180
TAATGGCTCG	CTCCAGAAC	TTCCGGAAAC	CCCAGTTGC	TCATCAATAT	GTAGCGAGTA	240
CTCATCATGC	GAGGGTGCAG	CGATCTGAA	ACGTACCTTG	TACGTACCAA	GCCCCTCTTC	300
AAACTTCACT	TCGCCCCATA	ATGCGGACCG	TCCCCTGCGT	TCAGGGGGGA	AACATCAACT	360
TTGCAACTTC	TCAGAGCCAT	GT TTTGGGGG	GAAGCAAAAA	ATT CGGGAT		409

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

GTTCGGAAA	TGCATGCAAT	GTCATGTTA	CAAATACAAA	TATCATGTTT	TCTCAGGTTT	60
CTAGAGCCTT	CTTCCTAGAA	AACTCGAATG	TGTGGAGGCT	TTGACTCCAG	GTGGAACCAA	120
TTAGCGTTG	GCAGCTAAAA	ACAAAACCTT	ACATGTTAAA	ATGCATTTGA	AACCTTAAAG	180
TCCATAGAGA	ATTTTGAGA	AAACACAAAC	ACACAAAGAG	ACTGTAGCAA	GATCTGGGAT	240
TGAGATAGCT	GAAAATCACC	AGATAGTTCT	GTTTCATCC	AGGAGTATCT	GGACAAATTG	300
TTGTGGATT	TGGTTGAAAT	TTAACCAAAA	ATAACCGTGA	CAGTGGTTTT	GGAGAAAAGC	360
ACAATCTTC	AGTTCGGCAA	ATGAATCCAA	TGCCATGTTT	ACAGAAAGAA	ATATCATGTT	420
TTCTCAGnTT	CGGAGCTTCT	TCCTAGAAAA	CTCGAATGTG	TGGAGGATTG	ACTCCAGGTG	480
GAACCAAAGA	GCGTTGCCA	GCTTAAACAA	AAAAGGGTCC	T		521

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

1063

TGCTGGGTGT TCTCTGTTTG TGTCTGCCGC TTCCCTACGAC GACAATGAAT TTTCTCGCAA	60
GAGTCGTGCG TACTCGGAGC TTGCAGAGAA GACCTACGAT GCGGGGAGAG TATGACGTCT	120
CTGCAGAGTA CGCCCCGGCTC GCTGAGGGTT TTGCGAAAAA ATCCTCGGTC TACATCAAGG	180
GAAACTATGG GCGCGCACCA ATGCCGAGGG ACGCTATGAA CGCTGCCGC ACCCGCCCAA	240
GCGTGGGGCG AAAAATTGAA GCGCATCGAn TGGCGCTATC CGACCGAGTA ATTGCTCGCT	300
AnGCGAnGGC TATCAAGACC GGAGGGCTTC GCTTTTGAC AnCCAAGCAG TACGACGTAG	360
CGCTTCACGT GGGGCGCGTn AAGGC GTTnG ACGCACTCCA AAAACGTAAA AnCTGAAAAT	420
TCATTGCTTG CCAAAGGCCG CGAAGGAAGA AGCTGCGCGC CAAGnCGCCG AAGCACGAAA	480
ACTCCGA	487

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

ATCnGTGTGC GTGCCGAGGA TGCACCAAGGT GTTATGTCC CCGnGAACCC TGCCCTCTCAA	60
GCACAGGATG CAGCGTTGA TTTCGATGGG GTGCACGTTA CGCGCGGAAC TAATTCTATC	120
ACCGACCTTA TCCCCGGCGT TACGTTTCG CTGCACGAAC GTACAGAAAA AACCGAAACG	180
CTCTCTGTCA CCCCCGACGT GAACGCCATG AAGAACGCTA TTATAGAATT CGTTGCTAAG	240
TACAATCGAC TCATGGCAGA ATTAACATT GTCACCAAGTA ACAAGTCAGA CCATTATnGA	300
CGAGCTTGC CG TGATCTTACC CCCGAGGAGA AAAAGAAAGA GACAGAACAA CTCGGnCAAC	360
CTCCACGGGG GAATCCA	377

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

CGTGCTTTCA CCTTTTCCCC ATTnAAGAG AGTGTAAATA TCCACAATAC GCTCACCATC	60
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1064

GTAGAACACA ATGACCTCTG AAnAAGGGTA CCGCCGCGTT GTAACTCCTG nnAATACGCT	120
TCCACGCTTC CACATTCCCG TTATGAAACA ACTCGTTAGA AACAGGCACC GATATTAACT	180
GAGACATCCG AATCGGACCT nCAGAGGCTT GAGCAGGAGG ACGCGCGGTG AGGGGGGGGG	240
GGGCAGACGA AnCCCGATCA CAGGTAGCCC CTTCAGACGC CCTGGnAGCG TCCGCACCCG	300
GTTCTTGCC GATCGAACCC TCTTGCCAGA ACCCTCAGAC TTTTCGTAG ACACAAATGC	360
nAAAAC	366

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

ATTTAAAAGG ATCTAGGTGA AGATCCTTT TGATAATCTC ATGACCAAAA TCCCTTAACG	60
TGAGTTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA	120
TCCCTTTTTCT CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACaCgCTA CCAGCGGTGG	180
TTTGTGTTGCC GGATCAAGAG CTACCAACTC TTTTTCCGAA GGTAACTGGC TTCAGCAGAG	240
CGCAGATACC AAATACTGTT CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT	300
CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG	360
GCGATAAGTC GTGTCTTACCC GGGTTGGACT CAAGACGATA GTTACCGGAT AAGGCGCAGC	420
GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT GGAGCGAACG ACCTACACCG	480
AACTGAGATA CCTACAGCGT GAGCTATGAG AAAGCGCCAC GCTTCCGAA GGGAGAAAGG	540
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG	600
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	660
GATTTTTGTG ATGCTCGTCA GGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT	720
TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTCCT GCGTTATCCC	780
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	840
GAACGACCGA GCGCAGsGgT CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC	900
GCCTCTCCCC GCGCGTTGGC CGATTCATTA ATGCAGCTGG CACGACAGTT TCC	953

(2) INFORMATION FOR SEQ ID NO: 598:

1065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

CCGAAGTAAC TGGCTTCAGC AGAGCGCAGA TACCAAATAC TGTTCTTCTA GTGTAGCCGT	60
AGTTAGGCCA CCACTTCAAG AnCTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC	120
TGTTCACAGA GATAACCCTTG CGTTTTTGCC AGGCGCAGTG CGGCAATGGT GTCAGCCGTT	180
TCTCCCGACT GAGnAAATCG TCAGTACTAT TTCACGCGCG TGCACGACGC TCGTGCATA	240
nCGGATACTC TGAGGCAATC TCCACCTGAC ATCCCACCCC TGCAAATGCC TCAAACCAGT	300
AACCGGCCAC TAACCCTGAC ATGGTACGAn GTACCACACG CGATAATGCG CACCCGTGTT	360
ATCCGTCTAA ACAGCCGCTA CAAACGTCTT ACACGAGGTA nCGTCCAAGA ChCGGTChTC	420
CCCGAACGTC CGCACCTGTG CGCGAGAAGA CGAAGAAAAGA CGACATAT	468

(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

GGAAGAGGCA CACCTGACAT GGAAGGAAGC TGCGCGTGC GCAAGTAGACG CAGGAGCACA	60
AGCGCTTGCG TTGCACCCGC GCACCTGCnC CAGTGTACG CGGGAGAGGC AAACCTGGGAC	120
ATAATCGCAG ACCTCGTGCA GTGGCGCGT GGGTGGGGAG AGGTTCCCGT GTTCGGCTCA	180
GGGGATCTGC ATGCGCCTGA AGACGCACGG GCAATGTTAG AACACACCGC ATGCGCGGGG	240
GTTATGTTG CCCGCGGTGC TATGGGCAAA CCGTTTATTT TCAGACAAAC CCGTCAAGCT	300
TTTAAACTGA AAGGATACTA ACACGCCCCG TGAACGTTTT GAAGCAAAAA GCTTAAGCGC	360
CAAATTGGCC GCGAACGCTTT CAACTTCTTG GCAACAAAGA ACGTTGGGA AGAAAAAGCT	420
TCAAGCCCTT GGCAAAACCA AGAATnTCCG CCAAAACGGT TTTTTTGGnT TTTCCGG	477

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs

1066

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CTCCAGAAAAC CTGAGAAAAC ATGATATTTC TTTCTGTGAA CATGACCTTG AATTCA	60
CTGAACACAA AGATTGTGCT TTTCTCCAAA ACCACTTCAG CGGTGATTTT TTGGTTAAAT	120
TTCATTTCAA AACTACAACA ATTTGTCCAG AGACTCCTGG ATGAAAACAA AACTATGTGG	180
TGATTTGTAG CTATCTCAAT CCCAGATCTT GCTACAGCCT CTGTGTGTGT TTGTGTTTTC	240
TGGATATTCT CTATGGACTT TAAGGTTTG AATGCATTTT AGCAGGACCC TTTTGTTTT	300
CTGCTGGCAA ACGCTAATTG GTTCCACCTG GAGTCAAATC CTCCACACAT TCGAGTTTC	360
TAGGAAGAAA GCTCAGAAAAC CTGAGAAAAC ATGATATTG TATTTGTAAA AATGACATGG	420
ATCATTGCTG AACAGAAAAGA TGTGCTTTTC TCCAAAACCA CTTTCACGGT GATTTTGAT	480
AAAATPTCAC CGGATATCCA CAAAAATTG TCCAGATACC CCTGGATGAA CAC	533

(2) INFORMATION FOR SEQ ID NO: 601:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

AAAACCACCTT CCACGGTGAT TTTGGTTAA ATTTCACCCG AAATCCACAA CATTGTGCC	60
AGATACTCTG GATGAAAGCA AAACTATCTG TTGTTTGTG GCTATCTCAA TCCCACATCT	120
TTCTACAGCC TCTGTGTTTG TGTTTCTGG ATATTCTCTA TGGACTTTAC GGTTTGAAT	180
GCATTTAGC AGGACCCATT TTGTTTCAG CTGGCAAACG CTAATTGGTT CCACCTGGAG	240
TCTAACACGC CACACATTG AGTTTCTAG GAAGAAAGCT TCAGAAACCT GAGAAAACAT	300
GATATTCCCTT TCTGTAAACA TGACATTGGC TGTATTTCCC ATACAGGAAG CATGAGTTTT	360
TCTCCAAAC CACTTCACG GTGGATTTG GTAAAGTTTC ACCCACAATA CACAACAATT	420
TGTCCTGGAT	430

(2) INFORMATION FOR SEQ ID NO: 602:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs

1067

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

GA	TTGAGCA	TGTCAAGTTC	TThCCCTGAA	GACGAGGGAG	GGGATGGTTC	TACCCTCACG	60
AGGAGACGAC	GGATTTGTT	GGCAGTGTGC	GCATTTCTCA	TTCTGCTCGG	TGGTGTCTTG		120
GTAGGTTGGG	TTCTGTACAT	GCACGGCGCC	TCTCGTCCTG	CGGTCTGCC	GTCACAAAAA		180
GTTGAACCTGG	CCCAGGTCTT	CTGGCGGCAT	GTTGCAGCCG	GTGAGCTTGG	AGCGTACTGC		240
GGTTGAGGCA	CGTGTTCGTC	GATCTCCAT	CTGAGACTGG	CTCTTCCAGA	AACCCACAAG		300
GGAAAAGGGA	CGTTCCCCCC	TGGCGTTCTT	CCCGGGGCT	GAAACGGGCT	AACGAGTGCA		360
G							361

(2) INFORMATION FOR SEQ ID NO: 603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGCGnGnAGA	GGATCCCGTG	TACAGTGTAA	ATGGCTGGTG	GTGGGATTAA	CGTAAACGTC	60
GTATGCGCCT	GTCACGTGGC	GCAC TGCTTC	CTCTATGC	CGCACGCACG	CAGnAAGCAT	120
ATACCGTGAA	CAACAAATGA	CACTTG	CATG AAAGACTACC	TCCTATT	CAG GGGTTTT	180
TTATGTATCC	AAAAGCTCTG	GGGAGGnAAC	GGCTGGCA	GACGGCAAGA	AACTTG	240
TACCGGTTAA	AAAACCGTAC	ACTTT	CATC CTATCTnGCT	GTGAAATGGG	AGCTAACGA	300
ATTATGACCC	AAAAAACTGn	CAAAAAATAG	TGCTGCCT			338

(2) INFORMATION FOR SEQ ID NO: 604:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

1068

CGGATnCCGA CTGCGTAATT TTGAATCGAG GAGTACAGTG ATGGAGACGT TTTTTACCTC	60
AGAGTCTGTG AGTGAGGGTC ATCCTGATAA GCTGTGCGAC CAGATTCTG ACGCTGTTCT	120
TGATGCCTGT CTTTCGCAAG ATCCTCACAG TTGTGTTGCG TGCGAAACTT TTGCTCCAC	180
GTCCCTTATC CTGATTGGAG GTGAAATTAG CACGCGGGCG CATATTAATC TTACCCAAAT	240
TGCGCGTGTGAT GTTGCCGCTG ACATTGGATA TGTAAGCGCT GATGTCGGTC TTGATGCAGC	300
GTCCATGGCT GTTCTTGATA TGACTCATCA TCAGTCGCCT GATATTGCGC AGGGGGTGCA	360
CGGTGCAGGA CTGAAGGAGT TTGCAGGATC GCAGGGGGCA GGGGATCAGG GGATTATGTT	420
TGGTTTGCG TGCCGCGAGA CGCCGGAGTT TATGCCCGCC CCCCTCATGT GCGCGCACGC	480
GGTTGTGCGC TATGCTGCCA CGCTTCGTCA TGAACGCCGT GTGCCGTGGC TGCCTCTGA	540
TGCAAAAAGT CAGGTTACCG TACAATACGA GGGACATCGA CCGGTACGTA TCAGTGCGGT	600
TGTGTTTCT CAGCAGCATG ATCCGTCACC TTCATACGAA ACCATTAGAG AAACGCTCAT	660
AGAGGAGATA GTGCGTCCGG CGCTTGCACC TACAnGTCTG TTAGATGAAA ACACGCGTTT	720
TTTATCAAT CCAACCGGTC GTTTGTCTAT GGCGGTCCCT TnGGGACAnT GGTTTnACCG	780
GGAGAAAGAT CATCGTAGAC ACGTATnGGG GAATnGGGCG CCATGGAnGA GGTCTTTCA	840
GTAAGGGTGC ATCTAAGGnA GATCGTCTGC AGCGTATATG CGCGTATATT GCAAAAAAAT	900
TTGGCAGCCG ACCTTCTGAC GCnGTTAGTG CAGCTTGCAT ACGCAATCGG GGTACAnAT	959

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

AGTATGCCCG CGCGGCAAAT GAAGACGnAA CGTGACGAAA CCCTCGTGCT ACTCAGTAAA	60
ACCCGAGACC CTGACCCGAC AGACCGnCAG CCGCAGACCG GCAGTGCAAC AACGACATCT	120
TATAGGATGG CAGGCGTACA TGCCCGTCCA CTACACGGTC CTGACCGGAC CCCAAGCCCC	180
AGCCGCAGCC AACATCAACT TCCCGGTATG GGGATGCCTC ACGCACATCG CAGCCAGCAA	240
TGTATTTCAAG GGAGTATTTTC TCAACATGGC CATGACCGGC ACACGACTGC GCCAGCCTCG	300
TGGGGCGTAA GAAAGACGGA GCGCAGGCAC CTnAGTCGAG GACTGCGTGA ATGTGGAAAnG	360
CTCGTTAGC TTCTCAGA	378

1069

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

CCACCCnTAT CAGTTACATC AATGGGAAAA CCATCGCACG CAGCAGCACG CAACAAGAAC	60
ACTTCCGAAT GCTCCGGCA CATATCGTGC GCAATACCCG CGCAATAAAC GTGCGGCTCA	120
AGCTGCGCTT CCAACGCATA CCGCCGTACC AGCATGCACC CAAACTCCGC TACACGACGC	180
GAATGCTCAT GCTGCACCGT CTCGGCAGTA TACGAAATAC CCCCACGCCT AATCTCACAC	240
TCTTCAACAG AAAAATACGG CGTTGTCCA ATTGCTAAAT GGAGCATCCG CACCCGATCG	300
TGCGCACTTG CACTTCCTTC CTTTCTTTG AAGGGGGAAA CGAnGTAGGC ACAAAACAGCA	360
CGCGGTCATA CCCGGCGTGC GGTGTACTGG CATCAGCAA GAGCAAGTGG CCCAGATGAA	420
CAGGATnGTA CGAACCGCCA AACAG	445

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GCCATTGCGCC ATTCAAGGCTG CGCAACTGTT GGGAAAGGGCG ATCGGTGCGG nnCTCTTCGC	60
TATTACGCCA GCTGGCGAAA GGGGGATGTG CTGCAAGGCG ATTAAGTTGG GTAACGCCAG	120
GGTTTTCCA GTCACGACGT TGTAAAACGA CGGCCAGTGC CAAGCTTGCA TGCCTGCAGG	180
TCGACTCTAG AGGATCCCCA GTCTTTTCAG ACTGTCCGCA TCATTGGCA AAACGATGAG	240
CGCAAAGTAC TTACCCGAGA CACTCGCCCA AGAGACAGGC GTATCTACCT GTTCACGTCC	300
ATCTCCTTCA GAGCATACTG TTTCGCCTGC CAACTGCACT ACCATGAAGT GCGAAACTCA	360
TATTGTCCGC CGCATCCGCT CAGGCCGAT CTCAGGCGGT GTGCGCAGGT ATAAnTGCTG	420
TCCCAAGTCA AAGCC	435

(2) INFORMATION FOR SEQ ID NO: 608:

1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

CTnCGGCAAC GCATACAAAA CACCGTCGnC GAGTTTTTC AACTGCGCGT CATTCTCCAC	60
AATTACGGTG CGTGCCTCTA CCGCACCGAG AATCTGACAC AAGATCACGC TCGGTAGCGT	120
CAGAGCCACG CGTGTACGTC TGCTGCACCA AGCGCCTGAA TACCAAAGCT CGCGTGGAGC	180
CACTCAACCC GATTGTCGGA AATCAAACCA ATGTCAATCA CCACGTACCA CACCCAATGA	240
CTGGCCAG	248

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

CAGAGGCTGT AGCAAGATTC TGGGGATTGA GATAGCTACA AATCACCAGA TAGTTTTGTT	60
TTCATCCAGG AGTTTCTGGA CAAATTGTTG TGGATTTCCG GTGAAGTTTA ACCAAAAATC	120
ACCGTGGAAA GTGGTTTGn GAGAAAAGCA CAATCTTCCT GTTTAGCAAA TTCATTCAAT	180
GTCATGTTCA CAAAAAGAAA TATCATGTTT TCTCAGGATT CTAAAGCTTT CTTCCCTAGA	240
ACACTCGAAT GTGTGGGAGT ATTTGACTGC AGTGGGACCA TTAGCGTTG CCAGCAGAAA	300
ACCAAAAAAGG GTCCTGCTAA AATGCATTCA AAACCTTTAA AGCCATAGnG ATATCCn	357

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA TCTTCTTGAG	60
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1071

ATCCTTTTTT TCTGGCGGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG CTACCAGCnn	120
GTTTGTTCGC CnnAATCAAG AGCTACCAAC TCTTTTCCG nAGnAACTGG CCTTCAGCAG	180
AGCGCAGGGG ACCAAATACT GTTCTTCTAG TGTAGCCGTA GTTAAGGCTC CCCACGnAAC	240
ACCGTGTTGC AGGCGTCAAG CGAATTGAAT ACCATGTTCT CTATCGCTGT TTCTGTGTTAG	300
AAGGCGATAT GAGGGGTATA GATGATACGC TCATGThCGA CAAnCCGAGC ATAGACCGTA	360
TCGTAATAGG	370

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

TGGTTAACCC CCCACCATTG GCCTTAACCC CCCAAGGCC CGGTTGGAA AAAAGGGACC	60
CACCCCTTAAT TCCCCCAAGG CCCAAGAGGG GGGGTTTAAC CGGGGGTTCC CAAGGGGGTT	120
CCCCCCAAAAA GGGAAAGGGAA TTGGGGGGAA AAAAAAAAGG CCCAACCCAA GGGAAAGnGG	180
GCCCAGGAAT TTGGGGGGAA ATTCCCCCTT TGGnTTTGGG CCCTTTTnA ATTTCCCAA	240
GGCCCAACCC GGGCCCCCA AAAACCCTTT AAAAAAAA AAGGTTTCCC CCCAAAAACC	300
CGGGAAATTG GGGAAACCGG GCCCAAACCG GGTTTnAACC GGGGAACCCn AACCTTTTT	360
GGGGAAACCTT TTTTCCCTT CCCGGTTTG GnCCGGTTT AAGGATTG GAAAAAAAAAA	420
AAAAGGGGAA AAAGGCCCGG GCCGGGCCCC CGGGTTAAA CCCAATTG nCCAAATTGG	480
GGGGCCCAAG GnCCGGCCCG GGGGGTTTnA AAAAAAAA ATTTCCCCCA AGGACCGGGT	540
T	541

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

CAATTTGTT GCGGTTATGG CTACGGnTGA nAGTACTTGC AGGAACCGGC CCACAGTTCA	60
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1072

GGAGGGCCTC GAAGGGGAGG CCCGGGTGA GTGCGCCGTC TCCTACGACA GCGACTACCT	120
TACCTGATT ACCCCGGTAT CGTAGGGCGC TGAGGATACC ACTTGTCGGG CAGAAAGTGC	180
CGTGGAAAGAG TGACCGGTAC CAAAAGCGTT CGTACGGGnC TTnCATACG TCGCCGCGGG	240
GAACCCCGnA AATCACCATC CTTCTGGACG GTAGGGTCAT GGGAAAGCGGC CCTGGCGCGT	300
GCCAGTGAGG nAGCTTGTGC GACGTACACT	330

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

TGGCTGTTCC ACTTCTGATC CAGCTCCCTG CGACTGGCCT GGGAAAGCAG AAGATGGCCC	60
AAGCGCTTGA GCTCCTGCAC CCACATGAAA GACCCAGAAAG CTCCTGGCTT CTGATCAGCC	120
CAACTCTGGc TGTTGCAGCC ATTTGGGAG TGAACCAAGTA GATGGAAGAA GATCTAACTC	180
TCCCTCTCTA ACTCTACCTT TCAAATAAAC AAATATTTTC TAAAAATTAA TACTTTGCA	240
AAAAATCTGG TCAGTTTATG TGGTCCAGA GTAATTATAA TATTGTTAGA ATTACTCTTT	300
ATTCTTAGTG TTTATTCTGC TGTATTGAAA TCACTTGGAC AGGATCTGGG AAGAAACCAG	360
CCAAGGAAAG AGGAAACAGA AGTAAACTCT TAAATTCTGT AATTCTTAAT AGATTATTTA	420
TTTGAGAGGC AGAGTTAGAG GAGAGACAGA AAGGTCTTCC ATCTCTGGT TCACTCCCTA	480
AATGGGCCAC AATGGGGCAG AATTGGGCC AATGGCCAGG GAACATCTTC CAGGTCTCCC	540
TTGTGGGTAC AGGGGCCAA GCACT	565

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

TGTGCCTTTT ATCTCTTCT GGCCCCTACT ACTCAACAAAC ACTGATTAA AAAAATTATA	60
TTGAAACAAAT ATCAATATTA GCGTTTTCT AGGTTTTTA CATGTGTTAT CTCACCAATA	120

1073

TTTACAAAGA AGATCCTAAA CAATACAGAT AACACCAAGA CCAAAAAAAA AAAAAAGTAA	180
TATATGCCAT TAGTTTAGAA ATTCAAACAA TATAAAAGAC ATAAAAAGCA AAAACAGAAG	240
CAACTTGGTT TCCATCCCC AAGGAAACAG CACCAACAAT TTTTTTTTTT TTTTTTTTTT	300
TTTTTTTTTA CAGGCAAAGT GGACAGTGAG AGAGAGAGAG AGAAAGGTCT TCCTTTGCC	360
GTTGGTTCAC CCTCCAATGG CCGCCGCGGC CAGCATGCTT GCAGCCAGTG CACCGCGCTG	420
ATCCAAAGCC AGGAGCCAGG CTGGCAACAG ATGGCTGCCA ACAGATG	467

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TTGCATGCCT GCAGGTCGAC TCTAGAGGAT CCCC GGTTTC GTACGTTCGT CTTATTTCCG	60
CGCGGGCATA CTCAGCAATA TTCTGCCTTC CACTTCGTAG GAGCAGCAGG AGCAGCAGGG	120
GGCGTGGCCT TTTTGTTCGT ACCGCCGTAC	150

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

TGCCTGGTT CAAGTCCTGC CTCCTCTACT TGAGTTCCG CTCATGTGCA CCCCAGGAGG	60
CAGCAGATGA TGCTGGCTCA AGTACTGGAT CCCTGTCCCC CATGTGGAG ACCCAGACTG	120
AGCTCTGGGC TCCTGGCTCC AGCCCTGGAT GATACAAGCA TTTGAGGAGT GAACCAGAAG	180
ATGGAAGATC GATCTCTCTC TCTCTCTCTC TTTCTCTCGT GTGCACACGC GCACGCATGC	240
TCATGGCCTG TCAAATAAAG TGAAAAAAGA AATCTGTGCA CCCAAGATTT ATGCATCTAT	300
ATATGTAAAC TTTCCTTCAA TTAAGAAACA TTAGGGGTCA GCATTGTAGC ACAGTGGGTA	360
AAGCTGCCAA TCGTGACACC GGCATCCCAT GTGGGCGCCG GTTCATGCC TGGCTGnCTC	420
CACTTCTCAT CCAGCTCCCT GCTAATGGCC TGGGAAAGCA ACAGGTGATA ACCCAAGTGT	480

1074

TTGCGTCCCT GCCACTCAGG TGGGAGACCC AGATGAAGCT CTTGGTTTG GCCTGGCCTA	540
GCCCTGGCCA TTGAGGGCCA ACAGGGCA GT GAACTACCAG TTGAAAGGTA TCATGTGCAC	600
TGGGCTCTCA CGC	613

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

GTGGGTGCAG GGGCTCAAGG ACTTGAGGCA TCTTCCACTG CTTTCCCAGG CCATAGCAGA	60
GAGCTGGATT GGAAGAGGGAG CAGCCAGGAC TAGAACCGGC ACCCATATGG GATGCCGGCG	120
TTTCAGGCCA GGGTTTTAAT CCTCTGCACC ACAGTGCCAG TCCCAGTGTGTT GCAATTGGA	180
TTGGTGTnGA CTTCAAG	196

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

GTATTTGAAA GCCAGAGTGA CAGGnGGGAG AGAAGGAGAG AAAGAGAGAA AGAGAGAGAG	60
AGAGAAAAGAG AAAGAGAGAG AGAGAGACTG CCCATTCTT GGTTCACTTC CCAAGTGGCC	120
ACAAGAGGCCA AGAGCCGGGA CTGGGCCAGG CAGAACCCG GAGACAGGAA CTCCATACAG	180
GTCTCCATG TGGGTGACAG GGGCCGAGT ACTTAGACCA TCATCTGCTG CTTTCCCAGA	240
CACATTAGCA GGGGACTGGA AAGGAAGCAG AATAGCCAGG AATCAAACCA GTACTCATAT	300
GGGATGTTAT TATCATAGGC AGTGGCTTAA CCCACTGTGG CCACTATGTC AGCCCCATAA	360
CTGGGCTTTT TTATTAAGC AGACACATTT TGCGCTGCC TGTCTACCTC TTAATCTACA	420
TTTTTTCATC ACAGCATAAA GAATTGTCTT TATTCATGTA CTCTCCAAAG CCTAACTAAA	480
TAATCATATA TTTAAATAAT TCATCAATAT AGACAAGCAA GAAATTTAT CTTCAGAGAA	540
TTTATGTGTT ACCATAAAAG AGAAGAGAAT GGGGCAAAAT GTGTCCAAA ATCTTATCCT	600

1075

603

TTT

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

AGAGCGGTCT TCCAACCATT GGPTCACTCC CCAGTTGGCC GCACCGGCCA GnAGCTGTGC	60
CAGTCCGAAG CCAGGAGCCA GGAGCCTCCT CTGGGTCTCC CATGCAGCTG CAGAGGCCA	120
AGGACTTGGG CAATCTTCTT CTGTTTACCC AGGCCATAGC TGAGAGCTGG ATCGGAAGTG	180
GAGCAGCCAA GACCCGAACC AGTACCCATA AGGGATGCCT GCACTGCAGA TGGCAGCTTT	240
ACCTGCTACA CTACAACGCC GGCCCCATCT TTCTTTATTA TTGAAGTATA GGAGCTTTA	300
TATGGTATGG AGACCAGTTC CTTGTCAGAT ACATGGTTG TAAATATCTC CTGTTCTGTA	360
GGTTTTTGCG TTTCTTGTAT TTTTGAAAT ATAAAAGTTT TTTAATTTG ACATCTGATT	420
TACCTACTTT GTGGTGATGG TTATACTTTT GATATTATAC CTAACAAACC AAGTCACAAT	480
CCAAAGTTAC ACAGATTTAT ACCTGGTTTT CCAAGAATT TACTGTTTTA GCTTTTTTA	540
TTTTAAAGGn TTATTTATTT ACTTGAGATG CAAAGTTATA G	581

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

CTTGAAGGGG TGTGTTTCT CAGATCATTT GGAAAATTC TTCCATAGAT GCGTGGTATT	60
ACTAGCACTC TGTGTGCAAG TCATTCTCTC TTTTTTTTTA AAAAAAAAGAT TTATTTATTT	120
ATTTGAAAGG CAGAGCAACA GAGGAACAA GAGACAGAGT GAAAGACAGA GAAAGAGATC	180
TTCCTTCCAC TGGTTCACTT CCCAAATGGC TACAACAGCA GGGCATTGGT CTAAGCCGAA	240
GCCAGGAGCC TGGAACTCCA TCCAGGTCTC CCACGTGGGT GGCAGGAGCT TCCACTGCTT	300
TCCCAGGCTC ATTATGAGGG AACTAGATGT GAAAAGAGCA GCTGGGTCTT GAACTGGTGC	360

1076

CCTGATATGG TTTGCCAGCA TCACAAAGTT CTGACTTAAC ACACTGAGCC ACCATACCAAG	420
CCCCTCAATC ATTTCTTTTC CCTATTGTGC CTATCTGTCA TACATTCCCTT TTGCTTATCA	480
TGCATTTGTG TGCTTTGCAA CAAACTGATT AATTCAAGGAA CTGTCTTTAA CTCACTTGCG	540
TTGTGATTAG ATTAAAGGGT AAAGGGACCT GCCCCTCCTA GAT	583

(2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

TGTCACTCCT TAAATATATA ATAGTAATTA TTATTTAAAG ATTTATTTAC TTATTGGAAA	60
GGTAGAGTTA CAGAGAGAGA GAGGGTGAAA CACAGAGAAA GAGAGGTCTT CCATCCACTG	120
GCTCACTCCC CCAATGGCCA CAATGGCTTA AGCTGGACTG GTCAAAAGCC AGGAGCCAGG	180
AGCCAGGAAC CAGGATCTTC CTGCGGGTCT CCCATGTGGG TGCAGGAGAC CAAGCACCTG	240
GACCATATTC CACTGTCTCC CAGGCACATC AGCAGGGAGC TGGATTGGAA GAGGAGGCAGC	300
CAGGACTCAA ACCAGTCCCC ATGTGGGATG CCGGCACAC AGGTAGAGGC TTAACCTAAT	360
ACACCAACAGT GAGAGCCCCCT AATTATTATT TTTATATTAA AAATAAAACT TAAAAGAAAA	420
GACATACAGA TAGGAAATAA GCATTGAAAA ATATACTCAA CATCATTAGC TATTAGGAAA	480
ATGCAAATTG AnATCCCAAT GAATATGACT GAACATCTAC TTACAATGGA CATATTAA	540
ACCGCCCTTT GTGACATTCT GTGTATTTT CAGAAACCAT AGAATTGTAT A	591

(2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

GAATAAAATA ATGAAAGCAT ATCTTCTTTA GTCATGTGTT TTCTTGTGATTATATTGA	60
GGGGTTTTAA TTGTTCACCT AAATAAAGCA ATGTTTTATT GTTTGAGTG TTATTTAAAT	120
GTTTCTGTGA AATTTTCTA ATTTATATCA CACTTTTTT TAAAGATTAA TTTATTTGT	180

1077

TGTTTGAAAG GCAGAGTTAC AGCGAGAAAAG AGGGAGATAC AGAGAGCTCT TCCATCTACT	240
ACTTCACTCC CCAAATGGCC AGAGCTGGC CATTCCACAT CCAGGAGCTA GCAGCTTCCT	300
CTGGGTCTCC CACATGGGTG TAGGGGCCA AGTACTTGGG CCATCTTACA CTGCTTCCC	360
AAAAGCATTA CCTGGGAACC CGATTGGAAA TGGAGCTACC GGGACTCAAA CTGGTGCCAA	420
TATGGAATGC CAGCACCAACA TGCAATGGTT TTGCCCCTTA TATCACAGTT TTGTGTCTTT	480
CTGGCTTCCC TCTCTCCCTT TATCCTGTTT TTCTTTTTAA AATTTTTTTA GTTTTTTGnC	540
TTTAGACAG TGnTTTGTAC TTTG	564

(2) INFORMATION FOR SEQ ID NO: 623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

AATTGATTAA TTAAAAAAAT TATGTCTTCC TGGAGAATTG TTCCCATTGT TATTTGAAAT	60
CTGCCCTGTC TGAAATTAAC CTAGCTACTC TTGCTTTATT TATTTATTTG AAAGTCAGAA	120
TTAGAGAGAG AGAGATCTTC CTTCCACTGG ATGACTCCCA GATAGCTACA ACAGCCAGGA	180
CTAGGCCAGG CTGACATCAG GTGCTGGAG TTTCATCCAG ATCTCCATG TGAGTTGCAG	240
GTATCCAAC ACTTGGGTCA TCTTCTACTG CTTTCCCAGA CCATTAGCAG GGAGCTGGAT	300
TGAAAGTGGGA GCAGCTGGGA CACAAACCAG TGCCCATATG GGATGCTGGC ATTACAGACA	360
GCTATTTTAC ACCCTATGCC TCAATGCTGG GCCCCAACTn CTGCTTCTT TCAATTAnGT	420
GTAA	424

(2) INFORMATION FOR SEQ ID NO: 624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

GCCCGACTGT ATCATTCTT GAAGGTATAA TTTAAAGGC CTTTCTCTGG GAAGCTTCTG	60
CAGGTTGCAG ACAAGTGTAA TTCTGCCTTC CTTGTGCCCT ACTGCTTAGT TGAGCCCCTA	120

1078

TTTCAGCGCT CACTGCTGTA TGCTATCATT TACCTCTTIG CGTGCTGTG TTGCTCCCAG	180
GTCTGCGAGC CTCTGCGGTG CAGGCAGGGA CTGTATCTT ATTACACCTCT ACATCCATCA	240
GCAGCACCTA GCACAGGACC TGGTATTACA TGTGAAAGA ATGTGTTCA AGATTCAAAT	300
CAATTTTTG TATTGCTCT AACTTCAAT ATAACATCATG GTGCATGCTC TAAAACCTGA	360
GCCCTTAGC TCATAGAGAA TTTATATTAA AGTTATGAAT TATATAGATG TGTATGCATA	420
AACCTTGTTC TTTAACTGGC TGGGATCATC CTTTTTAAA GATTTATTTT ATTTATTTAA	480
AAGACAGAGT TACAGAGAGA GGTAGAGATA GAGACAGAGA GAAAGGTCTT CATCCATAGT	540
TCACTCCCCA AATGGGCTAC AGTGGGCCAG AGCCAACCCA ATCCAAAGCC AGGAGCCAGG	600
AGCTCTTCCG GGTCTCCAG TGGGTGCAGG GGTCCCCAnG ACTTGAGG	648

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

CAGGCTTGTA ACAGTTCTGT TTTATGCAAT GTCGGCGCAT TCAGTACTAT CGCTTTTGGA	60
CGCGCACCTG ACGCGCGCGC TATGCTTCA CACAAAAGAC GGGTAACCTT CGGTAACAAA	120
AACTCTTCGT GCTGCTGCAG TAGTTAGGC TCAGAGAACCA GTAACACACC CAAATGCGCA	180
GAGTGCAGGC CGCCATCTTT ACGCCGTAAC GAAAGGCCGC GCGCACCGCA GCCACTTGAA	240
ACCGCTCTAC TATAGAGTCG CCATAAGATT CCAAAAGTTC ACGCGTGCAGC GCATnCCGCG	300
TTCATACAG TAACATCCCC GTTCTGCAAG CAGGCGCGAG ACCACATTCT TCCCCGCACC	360
ACTTnCGACC GATGACACCA ATTAGTGGAC AAAACTCGCG CACAGCGAGA GCGTnAACGT	420
CAAACACGCA CCGTCCTCAA GTGTTCAGAA TGTGCTGAAC ACCCGATATT CCTGCGTATC	480
TTGCGCTGAC TACCCCTGTG CCTCACGCGC AGACGnCAAAGACGCTTCT GTGGCATACT	540
GTCGTGTCT GGCACGGTTG GGAATAAACT CACGCTTGAG ACGACACAGC CGTTGCGCTG	600
CTGTTTGCAT ATCCGCATCA AAAATCCAGG GCAACACACG CGAGCGCCGG TTTCCTGTCA	660
GTTCTGCGTC ATGAATTCT GGTAACACAA AACAAACGCC ACTGAC	706

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs

1079

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

CACTGGGCGC TGAGCTCCAC CTTCTCGAAG GGACTGAACG TCATCCCACC TGGTACTGGA	60
GCGCTCGTTC ATTCAACAGG TTGCCCGCGG GTTTAATAAT GTTAAAGCGA TTGGTTGTGC	120
CGAGCACGGA TGTGTGTGGT GCAAGCCAGG CGTGGGAACC GAGGGGGATG CGATACTGCA	180
CCACGCCTTC CCCAAAATTG GCATATTGAT AGTCCCAGGG GGCACAGCTC CATTcAGTTC	240
GTACCCCTcCG TTATTTcTGT AACGGATGTA GGTGAGGGGG ATGTACACGC GTGCTTCGAC	300
GCCGGCGTTC AGGCCGGTGA GCAGGTGGGT GTAGGGGTCA CCGCTTTGG TTTGAGCTT	360
AAGGAATCCG GCAAAATCAA AGTAGTGCAG ACAGTGTTA GCAAAGACGC GTTTGCCAAA	420
GATATTAGTG CCTGCGGTGG CAAAGTATAT GCCAGAAGAG AGCCACTTCC ACTGcATACG	480
CAgGAGCGCG TCTATGTTGA GCGCGTTCAT AGGTGCGCGC TCAAGGAAAG CGAGAACGTT	540
AGCAGTGACA ACTCTTGGAT CGGAAGAGCG GAAGACATCA CGTACTCCTT GCTCTATGTT	600
CGGTACAAGT TGCGATACAA GCGCCGCGAG CGCGCCAgGC TaGCACGGTT TGAATGGCGC	660
TGCCGAGCGT TCCTTCTGCA ATCAAAGCAG CAAGTCCTAC CATCTCTATG AGAGTGGTTT	720
GTTCGGTGAT TCCTGGTGGC ATCATGATAT TGGGGAAAGT TCTGCACGAG TTTTCCCTnC	780
CAACCCGTCT AAACACTTTT CCTTGnTTTG AGGATAGCTC TCTCTGGGT CTGAnGCATG	840
TGCGTTACTC TGGTGTGGn TAnCGCGTC GAAGGGCGAA GAAGAACCGG AACCCGGCGG	900
CCTGGTTCGA CGGTGAATCG GCCTCCTAAT CCCCACAGGA ATGGCGGTTT TGGTTTTTCG	960
TnCTTGGGAn GT	972

(2) INFORMATION FOR SEQ ID NO: 627:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

CCATGCCCGC AAGTACCCCC GCTTGCATCA CCTGCCTGCC CACTCACTCC CCCTCCTCTC	60
ACTTCTACCT CACCCCCCCC CACCCGTCTA GCCGCGTGTG ACTACCAGGA GAGGGTGACG	120

1080

CCGCACACGA	TGCGGCCGAT	TCCCTGGGTG	AGGCACTCGG	ACACCAGCCA	GGTACGGGAC	180
ATCAGAGAGC	ATACCCCTGTT	CCCAATCAAG	GGAGAATACC	GTCTTCTCTA	TGAGACTGGC	240
TGAAATACCA	GCACGCAGCT	GTGCACAGTA	CTCCTTGGTT	AGATAGGTAG	CTCCTACTGC	300
TCCACCTGCA	GCAGGGGCAT	TCAGGTGTGC	ACGGTTGGTA	GAGGCATGGA	CCGTAACGCT	360
TGGCTTCACC	CAGCCGTAAT	CCTGCACCGG	GATGCGATAc	TACACCACGC	CTTCCCCACC	420
ACCGGTGGAC	GGATATACTC	CTTTTCCTGA	ATGCCACGCA	CAGCCGTCCC	CCCGTTATTT	480
TTGTATAGCG	CATAGGTGAG	GGGGATGTAC	ACGCGTGTCTT	CAACGCCGGC	GTCCAGGCCG	540
GTGAGCAGGT	GGGTGTAGGG	GTCACCGCTC	TTAGTTTCGA	GCTTAAGGAA	TCCGGCAAAG	600
TCGCCACAGC	TTGCGATGGT	GTTATCTAAC	ACCCTGGTGC	AAAAACGTT	TGCCGGTGCT	660
GTGGCAAAGT	ATATGCCAGA	AGACAGCCAC	TTCCACTGCG	CCGTAAACAG	CGCATCGAAG	720
GCGACATTGT	AGGTGTCAAG	ATACAGACAC	ACGGCGCTGA	CTCCCATTAG	AAAGGCACGC	780
CATGCAGACG	CACGCAGGTT	CTGTATAGCC	TGACGTATCT	GCTCCCCCGC	GTCCAACGCA	840
TCCGTCTTCT	TCTTCACTTC	TTCCGTTACA	AACGTCTGAC	CCTCAGTGAA	AAACTTTGTA	900
GCCTCAGCCG T						911

(2) INFORMATION FOR SEQ ID NO: 628:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

GTACTCTGGT	GTTGGTTACC	GGCGTCGAGG	GCGAAGGAGA	AGCGGAACCG	GCGCCTGGTT	60
CGAGGGTGAG	TCGGCCTCCT	ACTCCCCACA	GGAGTGCTGT	TTTGTGTTTCG	TTCTTGGAGT	120
CTTCGGTACC	CTTAACGTAT	TCTGGTCCAG	TGTGGCATTG	CCTGCCAGCT	CCAACGTAAG	180
CAGCCGCTGA	CGGTCGACGC	CATAGGAAAG	CGTTGCATCG	GCCCCGAAGC	CATACTTGCT	240
GTGCGTGGTG	TCAGTACTAT	CCCAGGCACC	ATTGGAAAGG	AAGGAGAGGA	AACCGATGTC	300
CACATCTACT	CCGCTGTTTC	CCACATTGTG	GGGCCTGGTA	GCCGAGTTTT	GACCCCGGAG	360
CCGGAGAAC	CAGGGGGCAT	AGCGAGTGTC	CTTTTCTGGA	ATAGGACACG	GGTGACAAAG	420
GGTTTCCACA	GCTGGGGCAA	AGTTAACACAC	ACAGGGAAAGG	ACTGGTACCC	ACTGTTCAAGG	480
TAGGCCCAT	AACAGTGCAG	GGTGCCTGG	AAGGAAGCGG	TAGGTTGGT	AAAGGACAGG	540

1081

GCCGTTGAGC TTTTACAAGA CGCAAGCTCT ACTGCCAGGT CCTTCAGCTG CAGCTGTGCC	600
CCACACCCCT GAGCGTGGCC TTCCCCCTC	628

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

CGGATACCCC TACTACCATG CAGCGTATT A CTGCTGATGT CACCGGTGAT GTGACCGTCT	60
CTACGGTGAA TCTACCCAGT GAAGAAATGA AAGGACGCAT CATTGGCGC GAGGGACGTA	120
ATATCCGCGC GTTAGAGACA CTCACTGGTG CTGACGTTGT CGTAGATGAC ACACCTGAAG	180
CTGTCGTCA TTCCCTGTTTC GACCCGGTAC GCAAAGAGAT TGCGCGCATC TCTCTTGAGC	240
GTCTTGTACT TGACGGTCGA ATCCATCCGG CGCGCATTGA GGAAATTGTG CAGAAGGTGA	300
CGCAGGAAGT TTCTCAAAAA ATCTATGAGG AAGGGGAGAA AGTGCCTGTT GACCTCGGTA	360
TTCACGATAT GTGTCCCGAG GGGGTACGGG CACTGGGGCG CCTGTATTTC CGTACAAGCT	420
ACGGACAGAA TGTACTCTAC CACTCAAAGG AGGTGGCTCT GCTCGCTTCC ATGCTCGCCT	480
CGGAAATCGG CGCAGATGTT GCCATTGCCA AAAGGGGGCGC GTTGnTGCAC GATATTGGCA	540
AGGGAATGGA AACTGATTCGA GACCGCAAnC ACGCAGAAAT TGGTATGGAG ATGGCTCGCA	600
AAATGAATGA GGACCCGGCA GTGGTAAACG CCGTTGGTTTC TCACCACAAAC GACATAGAGn	660
CGTGTGTGT TGAGTCnTGG CTCGTTCAAGG T	691

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

GTCCGTGCTC TGCAGGGGAA ACTTGGTCG CTGACCATCA TCGCGTTGCC CGTTATCGTA	60
GCTGTTGTCG CAGGGGGTGT CGGCTCCTTT TCCCTGCCCT ACGTAAAAT GATTACGCTT	120
TTCGTCGGCA GAGTTATCGC CACGTTCATC GCGCTCCAGC CATTACTCAT GAGTATCCTG	180

1082

CTGTCCATGT CTTTCTCGCT CATCATCATC TCCCCTGTGT CTTCCGTCGC GGTAGGAATC	240
GCCGTGGGGC TCACCGGTCT GGCAAGTGG A GCAGCAAACA TCGGCGTCTC CTCCTGCGCC	300
ATGACCCTCA TTGTGGGAAC CATGCCGTC AACAAAGATCG GTGTTCCGTT GGCATGTTTC	360
GCAGGAGCGA TGAAAATGCT CATGCCAAAT TGGATCCGGT ACCCGATTCT CAATATTCCG	420
CTCCTGCTCA ATGGCCTCGT TTGCGCGTG CTCGCGTGGC TTTTCAATCT GCAGGGTACT	480
CCTGCAAGCG CAGGCTTCGG TTTTATTGGA ATTGTTGGAn CGATCAACGC CTACAGGCTT	540
ATGGCGTAAA ACTCCTATGG TGCGCGCGGG TATTCTTTTC CTCGTGTATT TCGTTCTTTC	600
CTTCCTTGG CTGCGTA _n CT TAATGAnTTT AT	632

(2) INFORMATION FOR SEQ ID NO: 631:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

CCACTCGAGC GCGAGCATGn ACAGTTTTCG TACAGGTAGC GAAGTCTTAA GGTATTTAGC	60
GCACAGAACG CTGTTTCCGC AGCAGAGAAC AACATGGAAA GCACCAGCAG CACTACCAAC	120
ACACCGAACG CAGCGGAAAC GGAAAGAAC A CTCACACGTA ATTCCCCCGA AGGCTAAAAC	180
ACCAAGAACG AAGAGAACAC GCCATACATC CTTGGACCCC TCCCCGCTGG GGGGGGGCAC	240
CTTTTAAGGT GCTCACGCC C TTGTGTCAAG AGCACACCCCT CCACATACAAT GAACTGCGTG	300
TCCGGAGACC GCGCGGAGTC CTCTTTCTAT GAATAGAACCC GAATCTCCTC GTGGCTTAAT	360
CAAAGCCACC GTACGTGAAC AAGACCGAGG CCGAACCGTT TATAAAAAGA TTGCCCAGTT	420
CCTCTCCCTC ATTGGAGAACAGCAGGGCGG GCGCTGGTGC TCAAGCAACT TGAGCCTGCA	480
CAGATTGAGG CGGTGGTTGC CGAGCTCCTG ACACCTAAAC CCCTCAGTCC AGAAGAAGCG	540
CGTGAGATCC TACGGGAGTT TTCTGCCCTC TGCGCTCGTG TGTGCCTGT TACCGGTGGA	600
CTGCGTGCTG CGCATCGAT	619

(2) INFORMATION FOR SEQ ID NO: 632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 649 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

ATCCAATAGC AGGAGCCAGG AGCCAGGTGC TTTTCCTGGT CTCCCATGGG GTGCAGGGCC	60
CAAGCACCTG GGCCATCCTC CACTGCACTC CCTGGCCATA GCAGAGAGCT GGCCTGGAAG	120
AGGGGCAACC GGGACAGAAAT CGGGCGCCCC AACCAGGACT AGAACCCGGT GTGCCGGCGC	180
CGCAAGGTGG AGGATTAGCC TATTGAGCCA CGGCGCCGGC CGAAGTATTG AAGAAAAAAG	240
AGGGAAAGAT GTCTCACAGG ATGTCAAGAT TTATTCGATA GACTCATAAA TGCACAGTAA	300
GTAAAGTCAT TTGATGTTAG TGCAAATAGA CAAGTAGAGC TTGAACAGCA GGAAAGAGAA	360
GGAATAAnGn AnGnAGGnGG AGGAAGGGTG GAATGTGGGT GGGAGTCAGG GAGACCTTAA	420
ATTAGGAGAG GGTGCTCCCT GGGGACAGTT TTGTGTTACA GCAGGTTAAG CTGCCACCTA	480
GGATGTCAAC AGCACATATG GtGCCAGTTC CAGTCCTGGC TGCTCCAATT CCAATCCAGC	540
TCCCTGCTAT GGCCCGGGAA ATAGAAGAAG ATGGCTCAAG TACTTGGGCT CCTGCACCCA	600
GGTGGGAGAC CTGGAAGAAG CTCCTGGCTC CGGGCTTTGG CCTGGCCCA	649

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

GTGTGCCTGC TTCACCGCTC CTTCAAGCGAT CTGAGTAATA ACTGATCTTG CCACCTGCAC	60
CGAGTTATCT ATGGTGCTAC CAACCGTATC AGCCGCCTGT TTAGCCTGTT CCTGCGCACG	120
TGCGTAAAAA TTGCCAGTGC AACCTCCTGT GCACGCTCGC GTGTCCCTTC GGTCTCATC	180
GCCGCGGTAG CCTCACTCTG GTGTTGGTTA CGGGCGTCGA GGGCGAAGGA GAAGCGGAAG	240
CCGGCGCCTG GTTCGAGGGT GAGTCGGCCC CCTACATTCC ACAGCAGTTT ATCCTTGTTC	300
TGATTGTTTG CGTCCTCTG TGGCACCGAT GAGGTATCCG TCTTCTAGCG TAACATTGGC	360
TGGGCAAGCT CTACCGTGGC ACAGAGGGTG TCCTGGCAnG CGCATAACATT AGCTTCAAGT	420
CTGCCCAAA GCCATACTTT ACTGTGCGTG GGGTCAGTAC TATCCCAGGG CACCGTTAGA	480
GGCAAAGGAG AGAAACCCCA CATCAAGGCT GACCCCCACTG GCCCCCAATG TCCTGTGCC	540
GATAACCAAC CTTGCCGCCT AAACCCCCAA ACCCCGGCGC ATAATGTAAC GCATCCTCCT	600

1084

GGTATGCCGT G

611

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

CGGTATGGCG TTGATCTCTT CGGTTCTGGT GTTTTAGCCC TTGGGGGAA TTACGTGTGA	60
GTGTTCTTTC CGTTCCGCT GCGTTGGTG TGTTGGTAGT GCTGCTGGTG CTTTCCATGT	120
TGTTCTCTGC TGCAGAAACA GCGTTCTGTG CGCTAAATAC CTTAAGACTT CGCTACCTGT	180
ACGAAAAACG TCATGCTCGC GCTCGAGTGG CAATGCGTAT CCTTCGACGG AAAAACTTCT	240
ATCTTGCTGC TGTGGTTATC GGGAACACCC TGGCGAGCAG TGCCTTGCT GCAGTCATTG	300
CGCTTTTGC ACGTGCCTC TTTGGCATCC ACGCATGGAG nTGGAGCATC GGTGCAGGAA	360
CGGTGGCTTA CACTTCTTT TGGAGAAATT ATTCCGAATC ACTTGCCTTG TGCCGGCCGA	420
ACGCATGnCA CTGCATACTG CGCGATTCTT GCAGTGGAGC GCTTTGATGC TTACTCCTT	480
TGTACAGGTG TTCTGTATGG GCGCGGATGC GCTCTTGGGT CTTGGCGGTG TCGGTGCCAn	540
ACTCCCTCGC TGCCTGTTAG GGATGACGAC CTGCACACCG T	581

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

ATTAGGTGGG AGACAGAGAA GCTTGGCCGT CAGTTnAGGC GGAGTCAACA GTGAAATACC	60
ACCTTGGA CGTCAGGTTT CTAACCTTTG GCCGTGGATC CGGCAAAGGG ACCGTGGTAG	120
GTGGCGGTT TGACTGGGGC GGTCGCCTCC TAAAAGGTAA CGGAGGTGCG CGAAGGTCTC	180
CTCACACCGG TTGGAAATCG GTGCGCGAGT GTAAAGGCAC AAGGAGGCTT AACTGCGAGA	240
CCGACAGtCG AGCAGAtACG AAAGTAGGTC TTAGTGTATCT GGCGGTAcGT GTGGAAGCGC	300
CGTCACTTAA CGGATAAAAG GTACTCCGGG GATAACAGGC TGATTTCCCC CAAGAGTTCA	360

1085

CATCGACGGG AAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGAAGCAGG	420
TCCCAAGGGT TTGGCTGTT TC GCCAATTAAA GCGGTACGTG AGCTGGGTT AGAACGTCGC	480
GAGACAGTTC GGTCCTATC TGCTATGGGC GTTGGATATG TGAGAGGAGC TGCTTTAGT	540
ACGAGAGGAC CGAAGTGGAC GAACCTCTGG TGTACCAGTT ATCCTGCCAA GGTACGTGCT	600
GGGTAGCTAT GTTCGGAAGG GATAACCGCT GAAGGCATCT AAGTGGGAAG CCCGCCTCAA	660
GATTACATAT CCCTGAAGGT TGACCTTCCT GAAGACTCCT GCACACTACA AGGTCGATAG	720
GCTGGAGGTC TACGTACCGT AAGTATTAAG CCGACCAGTA CTAATAAGTC GTGAGGCTGA	780
CCATATTATC ATCCTTCCTCC TTCACCCCTAC CCCTTTGGGT AAAATATTTC GCCTGGTTGC	840
CAGGTGGAGA GGTACATACCC GTTCCC	866

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

AGGAGAnAA GGCGGACAGG TATCCGGTTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG	60
AGGGAGCTTC CAGGGGGAAA CGCCAGGGGT ATGCGGTAC CGGGGTTCGC ATCACGT CCT	120
TTGATGCGGA CGGGGTTCGC CACTCATT CAAGCGAGTT TGAACAGATT CCCCACGTAC	180
GGGAAGATAC CCTCGAGATT CTAATAATT TTAAGCGTCT GCGTTTCTC CTGCCGCAGG	240
GGCAGAGTCT AGTACGTTCA CGTATGAGTT TCGCGGCGCG TGTCTTGAC GGGGAAGGAC	300
TTCGCTAAGA AGTTTCAACT CGAGGTTCTG TCTCAAGACC TGCTCATCAT GGAAATGATG	360
GACGGTGCACG ATGTTGAAGT AGAGCTACAC GTCGAATTG GGCCTGGTA TGTACCTGCT	420
GAATCGCACG ATCGGTATGC CGATTTAGTT GGGGTTATCC CTGTTGACGC AATTTTTAGT	480
CCCGTGTGA GAGTCCGCTA TGATATTCAAG TCTTGCCGTG TAGGTCAGCG GGGGGATTAC	540
GATCAGTTAT CCCTTGAAGT GTGGACAGAT GGTACGGTGC GTCCCGAAGA CGCGATACCG	600
AGGCAGCGAA AATTATCAAG GAGCACTTTA CATTGGTTA A	641

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1086

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

ATAACCCTGA	TAAATGCTTC	AATAATATTG	AAAAAGGAAG	AGTATGAGTA	TTCAACATTT	60
CCGTGTCGCC	CTTATTCCCT	TTTTTGCGGC	ATTTTGCGCTT	CCTGTTTTTG	CTCACCCAGA	120
AACCGCTGGTG	AAAGTAAAAG	ATGCTGAAGA	TCAGTTGGGT	GCACGAGTGG	GTTACATCGA	180
ACTGGATCTC	AACAGCGGTA	AGATCCTTGA	GAGTTTTCGC	CCCGAAGAAC	GTTTTCCAAT	240
GATGAGCACT	TTTAAAGTTC	TGCTATGTGG	CGCGGTATT	TCCC GTATTG	ACGCCGGGCA	300
AGAGCAACTC	GGTCGCCGCA	TACACTATTC	TCAGAATGAC	TTGGTTGAGT	ACTCACCAGT	360
CACAGAAAAG	CATCTTACGG	ATGGCAGACA	GTAAGAGATT	ATGCAGTGCT	GCCATAACCA	420
GAGTGATAAC	ACTGCGGCCA	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	480
CGCTTTTGC	ACAAACAGGGG	GATCATGTAA	CTCGCCTGAT	CGTTGGGAAC	CGGAGC	536

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

CGTCCACTAC	ACGGTCCTGA	CCGGACCCCA	AGCCCCAGCC	GCAGCCAACA	TCAACTTCCC	60
GGTATGGGGA	TGCCTCACGC	ACATCGCAGG	CCAGCAATGT	ATTTCAAGGG	GTATTCTCA	120
ACATGGCCAT	GACCGCACAC	GAUTGCGCCA	CCTCGTGGGG	CGTAAGAAAG	ACGGAGCGCA	180
GGGCACCGTA	GGCGCGGACT	GGCGAATGT	GGAGGCTCGT	TTAGCTTCTC	AGACGTGTCG	240
GGGGCATTGC	ATCCGATGGT	GGCGCCATCA	AGCAGGGAAAG	TGCGCACTGG	GAGGGCAAAG	300
ACAGCAAGGG	CGTCGTTCCA	AGCAGGAGCA	AACCACAGCA	CGTACGGCGG	TAGAACAAAA	360
AAGCTGCTGC	TGCAGCCCC	GCTCCTGGTA	CGAATGGAGC	ACAAGAACAG	GACACGCGCG	420
CACTCCCTT	CACACAAAAA	ACCTCTTCCA	CGCCCGAGCC	CGAGCCGGAG	CCGCATGCCA	480
GCCGGCAGCC	GACGAnTTTT	ATAGGACGCA	GGCGTACATG	CCTGTCCATT	AnAAATCTAA	540
AAAGCCCACG	CCCGAGCCCC	AACGGAGATC	CAATTTCCCG			580

(2) INFORMATION FOR SEQ ID NO: 639:

1087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

TTGTATTCCGG TTCTTGGCGT TGTGTGGTGC TACAACTGCA TGTGCGCAGA ATCGTACGTG	60
TTCGGTTTGA GTTTCAAGGA TAGTAGGGAA GCGCGCGTGG CATAACCCTTT TCTGGTAGGA	120
TTGGAACCTCA TGTTCTTACT TGTGTGCTCG GCCCTATGTG CAGGTTCAGA AAGCGCGTTG	180
TCGTCGGTGA ACCAAGACGA TGAACGTAAG CTTAACCGGC ACAGTACACG TTGTACACAA	240
CGCTTATGCT GGCTTCTGGC CGGGCGCGAA CAGCTGATTA CCACAGTTAT TGTGCAAAAC	300
ACTGCACTGA ATATGGTGCT CTCTAGCGTG GTGACGTTAG GCTCTATGGA GTTGTGGGGT	360
GCACAGTnCG GTGTGGAAGG CACTGGTTGC GGTGACGTGC GTGATTATTC TTGTGGAGAA	420
ATGTTCCCGA AGGCGCTGGG TGCACGGTAC TCACTGGGAT TCTTGATGTG GATTGCGCCT	480
TTTTTGTAAT TGAGTTACTG GTTGCTGTAC CCCTGGCGCG TGTGTGTCGT CAGCATTGAT	540
GCATGTGCTG GAGGGTATTG TTTTGCCGCG TCATACGACG TGTCTTCGC GAGAAGAAAT	600
TAAAACGCTT ATTGCAGTTG	620

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

GGGCCAGTGC GTGGATTCTT CTGGAACGCA ATGCCCACT GGAGCTGGC TGTGCCACTG	60
ACCTGCGGAG TGAGTACGCC TGCATAACCA GAAGCAGCAC ATACCATGCC CGCAAGnGnC	120
CCCCGACTTG CATCACCTGC CTGCCCACTC ACTCCCCCTC CTCTCACTTC nACCTCACCC	180
CCCCCACCCG TCTAGCCGCG TGTGACTACC AGGAGAGGGT GACGCCGCAC ACGATGCGGC	240
CGATTCCCTG GGTGAGGCAC TCGGACACCA GCAGGTACGG GAACATCAGA GAGCATAACCC	300
TGTTCCAAT CAAGGGAGAA TACCGTCTTC TCTATGAGAC TGGCTGAAAT ACCAGCACGC	360
AGCTGTGCAC AGTACTCCCTT GGTTAGATAG CTAGCTCCTA CTGCTCCACC TGCAGCAGGG	420

1088

GCATTCAGGT GTGACACGGT TGGTAGAGGC ATGGACCGTA ACGCTTGCT TCACCCAGCC	480
GTAATCCTGn CACCGGGATG CGATAGTACA CCACGCCCTTC CCCACCACCG GCAGGCCAAT	540
GTGCCCTGAG GAACCGCCGG AAAGGAGAGG GTTCCCCTTA TTATTTTTGT ACAGGTCATG	600
GGTGAnGGGG ATGTACACGC GTGTTCAAC GCCGGCGTCC AGGCCGGTGA GCAAGTGGGT	660
GTAAGGGTCA CCCCTCTTAG TTTCGAGCTT nAGGAATCCG GCAAAGTCGC	710

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAGGTATCCG TACGCCACAT CCCCCTCAAT GCCCnCGGTT TCATTACCCC TGAnGCTGTA	60
CGTGCAAGCG TCAGTCCCCG TACCACGCTA GTTGCCTGAC GCCGTACATA GTGAAACCGG	120
CCGCCATCCA nCCGCTCCnn GnGATTGCGC ACGTGCTTGC ACATACAGGC ACACGCGGAC	180
GCTCTATCCA GCTCCACGTA GACGCCGCAC AGGCCTTTGG GAAAATACCG CTCAATCTGT	240
ATATGGACCT TCCGCGATA GAGGAACATG CACAGGAAA CAACGCGCCA CAGACACCAC	300
CGGGCTACCC CGCACCCACT GnACAAACGCG CGCTTACCTA CTCGGTAGCA ATCAGTGGCC	360
ACAAAAATAGG CGCACCAACGG GGTATTGGGC TACTGTGCCG ACACCGTTCA TTTACCCCT	420
TTGTCCTGGG AGGGGGACAG GAAnAAGAGn GCCGCCCCGGG AACTGAGAAC TTGCAGGTGC	480
GCTCGCGCTC GCnGCTTGCG TGTGCGAAAG CGCCTTCTTC CGTACTCTAC ATACCACTCC	540
GGAnGGCCCT ACACCCGCAT TACGAAGCCC ACAG	574

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

TATTGTTTA TTTTCTAAA TACATTCAAA TATGTATCCG CTCATGAGAC AATAACCCCTG	60
GATAAAATGCT TCAATAATAT TGAAAAAGGA AGAGTATGAG TATTCAACAT TTCCGTGTCG	120

1089

CCCTTATTCC	CTTTTTGCC	GCATTTGCC	TTCCTGTTT	TGCTCACCCA	GAAACGCTGG	180
TGAAAGTAAA	AGATGCTGAA	GATCAGTTGG	GTGCACGAGT	GGGTTACATC	GAACTGGATC	240
TCAACAGCGG	TAAGATCCTT	GAGAGTTTTC	GCCCCGAAGA	ACGTTTCCA	ATGATGAGCA	300
CTTTTAAAGT	TCTGCTATGT	GGCGCGGTAT	TATCCCGTAT	TGACGCCGGG	CAAGAGCAAn	360
TCGGTCGCGG	nCATACACTA	TTCTCAGAAT	GACTGGTTGA	GTACTCACCA	GTTCACAGAA	420
AAGCATTAC	GGGnGGACAG	ACATAAGAGA	ATATGCAGTG	CTGCCATAAC	CAGAGTGATA	480
ACACTGCGGn	CCAnCTTACT	TCTGACAACG	ATCGGAGGAC	CGAAGAGCTA	ACCGTTTTT	540
GCACAACAGG	GGGATCAGTA	A				561

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

CCTTATTCCCT	CCATTCTAAT	CACACACGTG	CATGCACCAA	GAGGACAGCG	CCGTGCTATC	60
TTCCCAGAAA	GGAGGATGAA	AACACGTGAA	AACCATTCTC	ATACTGGGTG	CAGGAACCAT	120
GCAAGCCCT	GCACCTCGCG	CACACGGGAG	CTTGGGCTGT	GGGTGTGCGC	GGTAGATGGG	180
AATCCGCATG	CACCGTGC	GGCACTTGCA	GACGAGTTTA	CCCCAATCGA	TTTGGCCGAT	240
AGCGCCGCGC	TCGTCGCTCA	CGCGCGCGCA	ATT CGCGCGC	ACGACGGCTT	GGATGCTGTG	300
TTCACCGCGG	CAACAGACTT	TTCCGTTTCC	GTCGCTGCCG	TCGCCGAGGC	CTGTGCACTC	360
CCCCGGCCAC	CGATTGGAGG	CAACCAAAAA	CGCTACGGAT	AAAACGCGCA	TGGTGGCCTG	420
nCTTCACACG	CGCCCGACTG	CGCTGCC	GCTTCACGTT	CCTTGAGCCT	GACTCGTTCG	480
CCTGGGGACA	CACCGCCTGG	GGCATGCCCG	ACTGTGTTCC	CACCTGCATA	GGCCTGGACT	540
CTCGTTTCC	CTCGTCGTA	AACCGACAGA	CAAACATGGG	AGCCCGCGGC	TGCACGCTCG	600
CGCAATGCAA	GGATAACCCTC					620

(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

TTCCCAGAAA GGAGGATGAA AACACGTGAA AACCATTCTC ATACTGGGTG CAGGAACCAT	60
GCAAGCCCT GCACCTCGCG CnACGGGGAG CTTGGGCTGT GGGTGTGCGC GGTAGATGGG	120
AATCCGCATG CACCGTGCAC GGCACTTGCA GACGAGTTA CCCCAATCGA TTTGGCCGAT	180
AGCGCCGCGC TCGTCGCTCA CGCGCGCGA ATT CGGnCCC GnCGGCTTGG ATGCTGTGTT	240
CACCGCGGCA ACAGACTTTT CCGTTCCGT CGCTGCCGTC GCCGAGGCCT GTGCACTCCC	300
CGGCCACCGA TTGGAGGCAA CCAAAAACGC TACGGATAAA ACGCGCATGG TGnCCTGCTT	360
CACACGCGCC CGACTGCGCT GCCCCCCTT CACGTTCCCTT GAGCCTGACT CGTTGCCCTG	420
GGACACACCG CCTGGGCATG CCCGACTGTG TTCCCACCTG CATAGCGCTG GACTCTCGTT	480
TCCCTCGTC GTAAAACCGA CAGACAACAT GGGAGCCCGC GGCTGCA	527

(2) INFORMATION FOR SEQ ID NO: 645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

TGTTCGGTGA TTCCTGGTGG CATCATGATA TTGGGAAGGT TCTGCACGAG TTTCCCCCTCC	60
ACCCGTCTAA ACACCTCCCT TGCTTTGAGG ATAGCTCTCT CTTGGGTCTG AGCATGTGCG	120
TTACTCTGGT GTTGGTTACC GGCGTCGAGG GCGAAGGAGA AGCGGAAGCC GGCGCCTGGT	180
TCGAGGGTGA GTCGGCCTCC TACTCCCCAC AGGAGTGCTG TTTtGTTTTC GTTCTTGGAG	240
TCTTCGGTAC CCTTAACGTA tTCTGGTCCA GTGTGGCATT CCCTGCCAGC TCCAACGTA	300
GCAGCCGCTG ACGGTCGACG CCATAGGAAA GCGTTGCATC GGCCCCGAAG CCATACTTGC	360
TGTGCGTGGT GTCAGTACTA TCCCAGGCAC CATTGGAAAG GAAGGAGAGG AAACCGATGT	420
CCACATCTAC TCCGCTGTTT CCCACATTGT GGGCCTGGTA GCCGAGTTTT GCCCCGGAGC	480
CGGAGAAACC AGGGGCATAG CGAGTGTCTT TTTCTGAATA GGCACGGGTG ACAAAAGGGKT	540
TCCACAGCTG GGCAAAGTTA ACCACACAGG GAAGnACTGG TACCCACTGT CAGTAGGGCC	600
CCATAACAGT GnCAGGGTTG CCTGGAAGGA AGCGGTAGGT TTGGTAAAGG ACAGGGCCGT	660
TGAGCTTTTA GAAGACGCAA GCTCTACTGC CAGGTCCCTTC AGCTGCAGCT GTGCCCACAC	720

1091

747

CCCTGAGCGT GCCTCCCCTC GGCGGGT

(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

GTGTATGTTG CCGGGTGTGG CGGCCGTGT TTCTCTCTCC CCCAAGCTCG GGGTGTACGG	60
GGACGCACGC GGCGGTTCTG ACCTGTGGGG CATCTGCATA CAAGCTCCCA CAATGCCAGA	120
TACAGAGAAC CAGGCGCCTC CGCGCTATGC CCGGAGACAC CGTTGGTGGG GCTGGACGTG	180
GCGTTCCGTG CGGAAAATGG CTTCCCTGCTC CAACTGACGG TGGACGCGGC ACTCACGCGT	240
TTAATGTTCT GCGGCCGGTG TTTGGCCGGT TATTGTTCA GACCGGGGGA AGTAGTACCG	300
CATCTGTCGG TAGCGGCCGGG TTTTGAGTGC ACCGCGCTCA TCTACGATAG CCAGCACTTT	360
CTTTCGGTTC TTGGGCAGGG CTTACTGCAG CCGAGCAGCT cGTCTTATTG AGCCGGTAAC	420
TGTCACCGCC CACGTTcATg CTTGGCGTGC TAACGTGCAC TGCCAAGGAG gTAGGCGCCA	480
TACACGAAaG aGTCGgCGTA TTAAAGGGGT CTGTCCAGAA CTATGGGGTG CCCGTGCAGC	540
TGGGGTACA GCACTATTTT AGCGCGCACT GGGGGATAGA CGCGACGGCT ACCGTTTCGT	600
TTGGCATTGA CACCAAGCTG GCTAAGTTCC GnATCCCGTA TACGTTGCGC TTTGGCCCCG	660
TCTTCCGCAC CTAGGGGACG GCGCTGGGAG GAAAGAGTCC TGCCGGAAGG CGCCTGCGGC	720
GGGTAGTAGC TACCAGGAGA GGGTGACGCG CACACGATGC GGCCGnCCCC CCCCCCCCCCCC	780
CCCTCGGACA CCAGCAGGTA CGGGACATCA GAGAGCATAC CCTGTTCCCA ATCAAGGGAG	840
AATACCGTCT TCTCTATGAG ACTGGCTGAA ATACCAGCAC GCAGCTGTGC ACAGTA	896

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

TATCCAAGTT CTGTTTGTGG GCTGCCTCGC GGTAGTCAAC AATACCAAAA ACGCTAAAGC	60
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1092

CCTGCGTGC	CAAAGCGCTT	CTCCAAAAGC	TGCATAGTGC	GATCGAAGGG	GTAGCGGCTG	120
GTGATCGTCA	TACGCACCCC	CGGCCGCGTG	TTGGAGGTTG	ACCCGGCTGC	GCTTGAAGTG	180
CAGGCAACAA	GCCCTCCTAA	AAGGAGCACT	CCCAGGGAAG	CAACCTTC	CCACACGCGC	240
CACCTGTGAT	GGCACAAACG	TCTACACACC	CCGCCTACCT	CCGCTGCGTG	TCATGCCCGG	300
CCAGATATGC	GCCGGCGCAA	AAATTGCCCC	CTTCGGAAAG	AAAAGAACCA	TACATCCCTA	360
CCAAATCAAG	CGACATGCC	CTACGAATTG	CCAACGCTCC	GTCACGTTCT	TCTCTATCAC	420
TACATTGCTG	TTCTCTTGT	GCTTGCCTTG	CTCCCAGCTC	AGCCGAATCT	CCACCTTCTC	480
TAACGGACTG	ACCACTACCC	CACACTCGTA	ATACCCACAA	TATTCCCTGC	TCCACTTCGT	540
AGCAGGAGCA	GCAGGGGGCG	TGGCCTTTT	GTTCGTACCG	CCGT		584

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

CACGTCTTCA	nnCCCCACCG	TAACCCCCAA	CGCAGCGTGT	GGCCAGTGCT	GCACCGGGCG	60
TTCTTGCCT	GTTCCCCCGG	CAGAATCAGA	TGCGTCTCCC	GTGGACCTGC	CAACCGAAAA	120
TAGAnATGGC	GATAACCCCG	GCGCTGTCCC	CTCAGGGCGC	GCGCCTGTCT	CTCCCACCGC	180
ACCCGGACAC	CGCTTTGGGA	ACAACGCCAT	AATTGCCCCT	GnATCCATAC	CCGCGTCCTG	240
GTGCACAGAC	GCACCTGTAT	CTGCCGGAAG	GTGCACGCGA	TGCGCGGTGT	CTTCCACAGA	300
AACCTGATT	CCCTCCCACA	AGAGAACTGA	GTTTGACTGA	CCCCACCCAG	GAGCGGACTG	360
CTCATGCGGC	GCATCCTGCG	GTTCTACAGC	TAGCTGCTGG	CAGGCAACnA	GAGCTGCACG	420
nAGTTACTTG	CCACGGnAA	AAACGCGGCA	CTCCAGGCGT	GnATAACGCG	CTTCCTGGCT	480
TCATTTCT	TTGGGCACGA	TGTAATCGTA	AATGTGCGCG	CTTAATCCTG	nnGCAACTGC	540
TGCAAGCGTG	GCCACGCACT	GG				562

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

CGGATACCCC GGAGAAATGC ACTTGAGTTA TTTGATGAAG CGTACGAGAA ACGGTATTTC	60
TCTCGGATTA TTGGCACAAA TGCGGTGTTTC CACACACAGC TTTCGCACAA GCAGTGGTAT	120
ACTGAAACCG ATGTGTCAGG GTTGTTCGCG CGCGTCATCG CnAATnTCAT CATAATCAAT	180
CGTTGAGCAG TCTCTTGGAT GATCGCAGTA TCATCGAGCG ACTCCTACAC GCTCGCTnGT	240
CCGTTGCGGG GACACCGCGC GCATAGGGTA GCGTCGCAAC GGACATGGGT TCGGGGATCT	300
TTGTCGCGGA CATCGGTACG TCTTCCCTAA AAGCGGCGAT TATTTCCTAA GATGGAAAGG	360
TGTTACAGTA CCAGCGCGTG TTCTTCCTC AGCCGGTGAA GGCCCAGGAT TGGGTGCGTT	420
CATTTTTTAC GGTGTTTGAG CGGTTGCGTG CCGTGCATCA CGTTATTGCC ATTACTATTT	480
CGGGCAATGG ACCGAGCGTC GTTGCCGTGC ACAAGAAGAG TCATGCCGAG GATC	534

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

GGGAGnACTG ATACGCCTAT TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC	60
GTCAGGTGGC ACTTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT TTTTCTAAAT	120
ACATTCAAAT ATGTATCCGC TCATGAGACA ATAACCCCTGA TAAATGCTTC AAAAATATTG	180
AAAAAGGAAG AGTATGAGTA TTCAACATTT CCGTGTGCGCC CTTATTCCCT TTTTTGnGGC	240
ATTTTGCCCTT CCTGTTTTG CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA	300
TCAGTTGGGT GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTA AGATCCTGAG	360
AGTTTTCGCC CGGAAGAACG TTTCCAATG AnGAGnACTT TAAAGTTCTG CTAGTGGACG	420
CGGTATTATC CCGTATGACG CCGGGCAAGA GCAACTCGTC GCCGGCATAAC ACTAATTCTC	480
AGAATGGACT GGTTGGAGTA CTCACCAGTC CAnCAGAAAA GCCATCTTAC GGATG	535

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

ACGCTTACCG AACGCTCCCC TCCAACGCGC TCAAATACTC CGTCTGGAG TACGCCGGAGG	60
AGCTTCGGTT GCAGTTCCAG GGGGAGATCT CCGACCTCAT CGAGAAAAAG GGTGCCACCG	120
TGAGCCAGTT CAAATCTTCC CCGATGGGTG CCGACCGCAC CTGAGAAGGC ACCTTTTCA	180
TGTCCGAATA ATTCGCTTTC TGCAAGCTAT GGACGAGTGC TGAGCAATTG ACGGGGACGA	240
AGGCTTGTGCG CTGCGGGTGG AAAGTTGGTG AACGGTTCGC GCAACAAGCT CCTTTCCAGT	300
GCCGGTTTCT CCACAAACAA GGACAGGGAG GTCAGAGGCT GCTACGAGCT TTATAGCATC	360
GAGTGTGCGT GTCCAAGCAG GAGAGGTTCC GATCATATT TTAAATGCAG TGATTGGGA	420
GCTAAGAGCG CATTTCGTTG GGTCAAAAGA GCGTGACTCT TTGACTCAGT GTCTCGGACG	480
CGTCGGTCTG GGCTACTGCG AGCGAGATAA GTTTAGAAAG AGTAGTAATG AAGCGTACAA	540
CGTCTGGGGT AAACT	555

(2) INFORMATION FOR SEQ ID NO: 652:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

AAAAACATAG CCATCTGCAA ATCAGTAATG AGACGTATAG GTGGTGACAC TGCCCGGTGC	60
TGGAAGGTTA AGAGGAGAGG TTCGTGGTAA CACAACGCTT TGAATTGAAG CCCCAGTAAA	120
CGGCGGCCGT AACTATAACG GTCCTAACGT AGCGAAATTG CTTGTCGGGT AAGTTCCGAC	180
CCGCACGAAT GGTGTAACGA CTCTGGACAC TGTCTCGACG CGAGACTCGG TGAAATTAT	240
GTACCGGTAA AGAAGCCGGT TACCCATAGT TAGACGGAAA GACCCCGTGA ACCTTCACCG	300
TAGCTTACTA TTGGAACCTTG GTTTACCATG TGTAGTATAG GTGGGAGACA GAGAAGCTTG	360
GCCGTCAGTT AGGCGGAGTC AACAGTGAAA TACCACCCCTT GGTACGTCAG GTTTCTAACCC	420
TTTGGCCGTG GATCCGGCAA AGGGACCGTG GTAGGTGGGC GGTTTACTG GGGCGGTCGC	480
CTCCTAAAAG GTAACGGAn GTnCGCGAA	509

(2) INFORMATION FOR SEQ ID NO: 653:

1095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

ACGCCCAGCG CCACCGCAGT CATA GTGCCG nTGTACACGC GCATGnCGTG GGTCCATGTT	60
AGGCCGATG TGAAACCACA TGGAGCCACC GATGACGTTTC TCACCTTCAn TGCGGGAGAA	120
GCGGCCGTG AGCAAGTTCA TGCCGTTGAA CTGGGCAGAA CTAGCGATGC GGnTCTACCT	180
CTGCCACAAG CTGC GAAACT TCCACCTGGA TCTGCATGCG GTCTTCAGCA GAGTAGATGC	240
CGTTTGCCGC TTGAATTGCA AGCTCTCGGA TACGCTGCAT GATGTCGGTG GTTTCTTGCA	300
GATAGGCTTC GGTAAACCTGA ATGAAGTTCA CACCGTTTGA GGCATGGTG GATGCCTGGT	360
TGAGGCCGCG GATTGGCTG CGCATTTTTT CTGAGACAGC CAAACCAAGAA GCGTCATCCC	420
CTGCGCGGnT GATGCGGTAC CGGATGAAAG CTTCTCGATG CCCTTCCAA CCTGGACATT	480
GGnGTGCCCG AGTGTGCCGT	499

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

TGGGGCGACG GCGGGTACAA TGTATTTGGT AAGCGCGTGC TGCCTGCGCT GCGGTCCCTGG	60
CATTTTGATT TTGCCGGATT CCTCAAACTC GAAACCAAAA GCGGTGACCC CTACACCCAC	120
CTGCTCACCG GCCTGAACGC CGGGCTCGAA GCACGCGTGT ACATCCCCCT CACCTACATC	180
CGTTACAGAA ATAACGGAGG GTACGAAC TG AATGGAGCTG TGCCCCCTGG GACTATCAAT	240
ATGCCAATTT TGGGGAAAGGC GTGGTGCAGC TATCGCATCC CCCTCGGTT CCACGCCTGG	300
CTTACACCGC ATACATCCGT GCTCGGCACA ACCAATCGCT TTAACGTTAT TAACCCCGCG	360
TACACCCCTGT TGAATGAACG AGCGCTCCAG TACCAGGTGG GACTGACGTT CAGTCCCTTC	420
GAGAAGGTGG AGCTCAGCGC CCAGTGGAA CAGGGGGTGC TTGCTGACGC TCCTTACATG	480
GGTATTGCCG AGAGTATGTG GTCTGAGCGT TACTTTGGCA CGTTTATCTG TGGGGTGAAG	540

1096

GTGGTTTGGT GAGGGGTTGT CGTGTGGCC AGAGAACGGG TACGGTGGGG GTGCGCGTTT	600
TCCCCGTGGG GCTGTGCCGC CTCAGTTTAC AGGCGA	636

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

ACAAGATGCC GCAAATCTTA AGGCTCGTT AGAGGCTCAG CCTGTGGTTA TTGCCATGCC	60
CGCCGGTACC AACGGTAAGT TGTACGGCGC TGTCACGAGT CATAACGTTG CAGAACAACT	120
TGCGTGCATG GGATTTGAGG TTGAGCGCAA CnAGTGGAGG TCCCTGGTCT TACTCTGAAA	180
TGTGTGGGA ACTATCACGT CACTATAAGA CTATACGAGG AAATATGTGC TGGTGTTCCT	240
GTCACCATCA AAAACCAAAG CGAAGGAnCA GTGTGAGTGA GTAGACCGTT TGCGGAAGTA	300
TCTCTCTGCA CGGAGTATGT GCTGTTCGTT TTTAGTTGTG CAAAGAACTG TGCCACTTTG	360
GGGCTGGATC CACGGAACGG AGACAGTTCT GGCAAGTGGG CCTCAACCCT TGCCCTCGTTA	420
GAGGTTTCCA CGGAGGAnGGG GGGGACTGTC TTTCACCACC TTCCCTCCTC TGAGTATTCC	480
TCGGAGGAGG TTCTGTGCCG GGCATGCCTA ATC	513

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

CGCGCACGGT GGTGACTGAC CGGACTCTCG TGCGGAnGAG AGTAGGAGTC TAAAATCTTA	60
TCAGGGGCTC CGGGTGGGAC TCCGGCTGCC AGGGCTCGGG CTTGGCGTG GACGGGCACG	120
CAACCCATAA GATGTTGGCT GGGGTTGGG CTGGGGGAAA TAGACGTGCG GCGTGCGTTG	180
GGCGATAACC CACAATATCC TGCCTTCCAC TTCGTAGGAG CAGCATCGTT TTTCTTGTTC	240
GTACCGCGCC TGTGTGCGTT TGTGCGCGCA nGTnCCCTGC TGCTGGGGCG CCCGTGTTTG	300
ACTTGCCCTC CCAGTCGGTG TGAGGCAGGC CGCGTCTATC CCTCAGTGCAG CATGTCCTCC	360

1097

CTGCTTGAGG GGTGGGGCGC CACCATTTTC ATATGCAATG CCCCAGATGC AGTCGTCCTT	420
CTGCATGGGT GTGGTGAGAA AGACACCCCTG AAATACATTG CTCTACTTCG TACCAGGAAC	480
TGCAGCAGCA GGGGAAACAG GGACACCTGG GTGAAAAGAC TGCACCATGC TAGGATGGGG	540
AATGGATATG TCCAAAAGTG TGA	563

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

GAACCCTACT CATATATACT TTAGATTGAT TAAAAACTTC ATTTTAATT TAAAAGGATC	60
TAGGTGAAGA TCCTTTTGTA TAATCTCATG ACCAAAATCC CTTAACGTGA GTATnCGTTC	120
CACTGAnCGT CAGACCCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG	180
CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGTT TGTTTGCCGG	240
ATCAAGAGCT ACCAACTCTT TnnCCGAAGT AACTGGCTTC AGCAGAGCGC AGATACCAA	300
TACTGTnCTT CTAGTGTAGC CGTAGTTAGG CCACCACTTC AAGAACTCTG nAGCACCGCC	360
TACATACCTC GnTCTGCTAA TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG	420
TCTTACCGGG TTGGACTCAA GACGATAGTA ACCGGATAAG GCGCAnGGAT CGGGCTGAAC	480
GGGGGGTTCG TGCACACAGC CCAGCTTGGA GCGCAnGACC TACACCG	527

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

CTGnCAGTTC CTGGTACGAA nAGAGGCAAT GTATTCAGG GTGTCTTCT CACCACACCC	60
ATGCAGAAGG ACGACTGCAT CTGGGGCATT GCATATGAAA ATGGTGGCGC CCAACCCCTC	120
AAGCAGGGAG GACATGCGCA CTGAGGGATA GACGCGGCCT GCCTCACACC GACTGGGAGG	180
GCAAGTCAAA CACGGCGCC CCAGCAGCAG GGACGCGCTG CGCCACAAAC GCACACAGGC	240

1098

GGGGTACGAA CAAGAAAAAC GATGCTGCTC CTACGAATGG AAGGCAGGAT ATTGTGGGTA	300
TGCCCCAAC GCACGCCGCA CGTCTATTTC CCCCAGCCCA ACCCCCAGCC AACATCTTAT	360
GGGTTGCGTG CCCGTCCACG CCCAAGCCCG AGCCCTGGCA GCCGGAGTCC CACCCGGAGC	420
CCCTGATAAG ATTTTAGACT CCTACTCTCC TTTCGCACGAG AGTCCGGTCA GTCAACCACCG	480
TGCGCGTATA TTCGGGGGAG TATTCTCAC CAATAACATG CTGCAGCAGC ACTGCGCAGT	540
CAGACGTGGG GCATAAGAAA GAGAATGCAG CGAACGTCAA TGGCACCGTG AGCGCCGGCA	600
CGCGGGGCA TTGCATCCGA	620

(2) INFORMATION FOR SEQ ID NO: 659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

CCGGTCTGCC TCCTGACGnA TCAGGTCTGC GGATGCAAGG GTCCGCGTGT TACCGTCTTT	60
GAGAGCAGAT TTTTGGAAATG TCTCGTTTT AATTGCGGAT TCAGGGAGTC GTTTTGCCTC	120
TTATATGCGG CGCACCCATG CTCAAGGGTT TnGGGAACGG ATGGGTCAAA TTATGGCGTT	180
ACCTTTTCAG CTGCATGATG CGTATCCCCC CAnCGTGGTG GGGAGAAGGG AGACAGCTGG	240
TAGAGGATCT TGCCCTTGAG GTGTGTGCAG GTCTGGAGTA TCTGGAGTCT GTGACCCAGT	300
TGCAACCGGT ATACACCGTT TCAGTGGACA nGCAAnGAT AGTCGTnGT TGCAGCTAAG	360
GCTGATGTCA TGGGGCGTTG TTTTGTGTTA CCAGAAATTG ATGACGCAGA ACTGACAGGA	420
AACCGGGCGC TCCnTGTGTT GCCTGGATTT GATGCGGATA TGCAAAACAnC AGCGAACGG	480
CGTGTGCTC CAAGCGTGAG TTT	503

(2) INFORMATION FOR SEQ ID NO: 660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

ATTCAGTTCG TACCCCTCCGT TATTCTGTGA ACGGATGTAG GTGAGGGGGA TGTACACGCG	60
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1099	
TGCTTCGACG CCGCGTTCA GGCCGGTGAG CAGGTGGGTG TAGGGGTAC CGCTTTGGT	120
TTCGAGTTG AGGAATCCGG CAAAATCAAA ATGCCAGGAC CGCAGCGCAG GCAGCACGCG	180
CTTACCAAAT ACATTGGTAC CCGCCGTCGC CCCATACAGT CCAGCCGACA CATAGGTCCA	240
CTGCGCCGTA AGCAGCGCAT CAGCATTGAA CCGGTCCAGC CGTGCACGCT CAAGCCAGGT	300
TAGCAGCATG ATAAGCACGA TGTCCGACTG ACTCGGCGCC ACAATCTCCT GTAGTCTCTG	360
CTCCGCCTGC GCCCTCTGGG GCAAGAGTTT TACCAACGCC ATTTGGATAA ACCGATCTCC	420
ACTATCAGTG GCAACCTTCG TCAGCGTAGA GACGAGCGTA CCGCCTGCA GCGTGAGGGC	480
AAGCCCCACC CGCTCGAGAA TCGAGGACTC CGCCATCTGT CnCAGCAAAA ATTCAAGATA	540
CTTATCCTTT ACACGGTAnT GCTCCAACCC TGAAGGAAAT CGAAACG	587

(2) INFORMATION FOR SEQ ID NO: 661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

AGGAAGTAAA AAAAGACGCT GCGCTGGTAC AGGTGCACC CCTGTTGCGC GCAAnAGACGC	60
AGACGTGCGC ACACATGCTG CACGCAAAAA AATGGTACAG GCGTTGCGCC TACACATGAA	120
GGTTTGTGCG CGTGAGTTAC GATTGAAAGA GGCAGCCCTC ATCCGAGACA AAATTTGCA	180
ACTGCAAAGG CAAGACGAGC AAAACGGGGT TTGATAGGGG AGGTGGAATC GAACAGCACG	240
CGTTTTTACC ATGTCACTTT CATTCCGCAG ACAAGGGTGC CGAAGTGGCG TTCGGACCAG	300
ATGCTCTCGG CAATGCCCAT GTAAGGAGCG TCACAAGCAC GCCCTGTTCC CACTGGCGC	360
TGAGCTCCAC CTTCTCGAAG GGACTGAACG TCAGTCCCAC CTGGTACTGG AGCGCTCGTT	420
CATTCAACAG GTTGCCCGCG GGGTTAATAA TGTTAAAGCG ATTGGTT	467

(2) INFORMATION FOR SEQ ID NO: 662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

1100	
GCCAAAGTAT GCTGCACCCC CAGCTGCACC GGCACCGCGT ATTCTGGCAA ATCCCCGTGA	60
TGCCCAATTG CTCAGACTCA GCCCTAGCAT CCTGACACTT CCGGCGCCTC AGCAGGCTCA	120
GCACTGTCTT TGGAACGTAC CACCCCTCCAT GTTCGAACGA ACACACCGAA CCCTCATTGG	180
GGGCCTGGAT GGTGATGTAA TGGTAGCTGT CGTAGATGAG CCCAGTGCAC TCAAAACCG	240
CCGCTACCGA CAGATACGTA TTTACCCCCC CCCGGCCTGA ACGAATAAnC GGnCAAACAC	300
TGACCACGGA ACATCAGGCG GGTGAGCGCC GCGTTCCACC GTCAGCTGGA GCAGAAAACC	360
ATTCTCCGCA GGAACGCCAC ATCGAGTCCC ACCAnCGGGG TCTCCGGCGC ATAAGGGGAG	420
TAATACTCCA TCTCCGTGTC ATCGGGATCC CCATTACCTC CTTGCATCGG TCGCCTTAAT	480
ACACAAGCCC CACAAGTCAA GAACGCCACG TGGGTTnCCA nAAGGCCCA	530

(2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

ATTCAAAGCG TTGTGTTACC ACGGAACCTC TCCTCTTAAC CTTCCAGCAC CGGGCAGGTG	60
TCACCACCTA TACGTCTCAT TACTGATTG CAGATGGCTA TGTTTTTGAT AAACAGTCGC	120
CTGGACCTGC TTTCTGCCAC CCTCACCAAA GGCAAGGGTC ACACCTCTCC CGAGGTTACG	180
TGTGTATTTT GCCGAGTTCC TTGACGCGAG TTCTCTCGAG CGCCTTAGAT TACTCATCCT	240
ACCTACCTGT GTGGGTTTGC GGTACGGTCT CTTGCAACCT AACCTTAGAC AGTATTTCCC	300
GTGCCATGTA CTACACCTGC TTCCCTTCGC TCATCGCTCC AGTCGCACTC GCACCTTACC	360
TCGAACGACG GATTGCTTA TCGCTCTTAA AAGGCTCGGG ATACTTAGAC CAAAACCTACC	420
AATCTTTGGC CGGGCTCAAC TCACGGTCCT GCCATCGAAA TGCAAGAGGT TCGGAATATA	480
AACCGGATTC CCATCGACTA AGACCCCTCGT CCTCGCCTTA AGGGGCGAnT AACCT	535

(2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

GCAGTGCCAG CCGCAGCCGA CGACATCTTA TAGGACGCAG CGTACATGCC TGTCCATTAC	60
AAAGTCCTAA AAGCCCACGC CCGAGCCCCA GCCGACATCC ACTTCCCGGT GTGGGACGTC	120
CGCCCGCATC GAAGGCCAGC AATGTATTG AGGGAGTATT TCTCGCTAGA AACATAGCCA	180
TGCGAGAGCA CGACTGCGCA AACCTCACGG GGCATTGCAT CTGAAAAAAA TGGTGGCGCC	240
CAACCCCTCA AGCAGGGAGG ACGCGTGCAC TGGAGCTAGG CGCACCCCCCT TAACACCGAC	300
TGGGAGGGCA AACCAAACGG GCAACGTTCC CAGCAGGAGT AACCCCCAGC ACGTTACGGG	360
CGGTACGAAC AAGCAAGCTG GCTGCGGTC CCCGGGCGTC GTCCCTGGTG GCGGTTCCCTG	420
GCTCTTACGA ATGGGGAGGC AGGAACAAGA CACGCGCGCA CATCCCCCTC ACACAAAAAA	480
CCTCGTTCCA CGCCCGAGCC GTACCCCCAG CCCGGAGTTG ACATCTACTT CTCGGGTCGG	540
CAGTCGCCCCG GAGGAACCTCC ACACTGTTCT AGCGGGTATG CCCAAGCAGC CGGGAGCCGG	600
CAACCGGGAG TTCCAGCCCT AACCGGGAGC CGGCAnCCCC A	641

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

TTTACACGGT ATTGCTCCAC CCTGAGGGCA TCGAACGCGC TGTCAAACCTT CTCCCGTGAG	60
CTCCCCGTTG CCAGAAGGCG ATTACCTGCA TCGGCAGGGT CCTGGTGTGTTG GTTACCGGCG	120
TCGAGGGCGA AGGAGAACCG GAAGCCGGCG CCTGGTTCGA GGGTGAGTCG GCCTCCTACT	180
CCCCACAGGA GTGCTGTTTT GTTTTCGTTG GTGGAGTCTT CGGTACCCCTT ACGGTAGTGC	240
TGCTCCAGTG TGGCATTCCC TGCCAGCTCC AACGTAAGCA GCCGCTGACG GTCGACGCCA	300
TAGGAAAGCG TTnCATCGGC CCCGAAGCCA TACTTGCTGT CGGTGGTGTC AGTAnTATCC	360
CAGGCACCAT TGGAAAGGAA GGAGAGGAAA CCGATGTCCA CATCnACTCC GCTGTTCC	420
ACATTGTGGG CCTG	434

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

GGGGGGTTCG	TGCACACAGC	CCAGCTTGGA	GCGAACGACC	TACACCGAAC	TGAGATACCT	60
ACAGCGTGAC	TATGAGAAAG	CGCCACGCTT	CCCAGAGAn	AAAGGCGGAC	AGCTCTTGCT	120
AGATGTTGCG	ACACGTAACC	GGTTTGTGCT	TTCGGATCCT	GCGCCGGCGG	TTTTGTGGAA	180
TGCCCTCGCT	GAECTGGGTA	TTGACGTAAC	GCTCCTGACC	TGGACTCACA	TTGAGCATT	240
CAATGATTG	CGCAATGCTA	TCTTCGTGGA	TATCGACGAA	TGCTTCAAAC	AGGCGGGCAT	300
TGAGGTTCCC	TTTCCGCATG	TGGACGTACG	GGTGCAGGGG	GCGTGCATG	CGCCACGTGC	360
GGAAAnGGTG	TGAAATGCAG	GGTGAGTCTT	GAAnGTGCGCT	TTTTCTTTGG	ACATTGACAG	420
GATGGATAGA	GGGACAGGGG	GAAGCCGAAT	GAGATGAAAG	AAAAAACGGT	GAGCGCTGCG	480
CTCGTAGGGn	AACTCATTGC	CCTAACGCTA	nGGGTGGTTG	CGTGTACTCA	GGTGAAGGAT	540

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

AGCAGGTGTA	TCATGGCGAC	GGGAAATACT	GTCTAAGGTT	AGGTTGCAAG	AGACCGTACC	60
GCAAACCGAC	ACAGGTAGGT	AGGATGAGTA	ATCTAAGGCG	CTCGAGAGAA	CTCGCGTCAA	120
GGAACTCGGC	AAAATACACA	CGTAACCTCG	GGAGAAAGTGT	GACCCTTGCC	TTTGGTGAGG	180
GTGGCAGAAA	GCAGGTCCAG	GCGACTGTTT	ATCAAAAACA	TAGCCATCTG	CAAATCAGTA	240
ATGAGACGTA	TAGGTGGTGA	CACCTGCCCG	GTGCTGGAAG	GTAAAGAGGA	GAGGTTCGTG	300
GTAACACAAC	GCTTTGAATT	GAAGCCCCAG	TAAACGGCGG	CCGTAACTAT	AACGGTCCTA	360
AGTAGCGAAA	TTCCTGTCGG	GTAAGTTCCG	ACCCGCACGA	nTGGGTAAAC	GACTCTGGAC	420
ACTGTCTACG	ACGCG					435

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1103

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

CCACCGCTAC CAGCGTGGTn TTGTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG	60
TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTTCT TCTAGTGTAG CTTGTGTATT	120
AAGGCGACCG ATGCAGAGGA GGTAAGTGGG GATCCCGATG ACACGGAGAT GGAGTATTTA	180
CCTCCCCGTT ATGCGCCGGA GACGCCGCTG GTGGGACTCG ATGTGGCGTT CCGTGACGGA	240
GAATGGTTTT CTGCTCCAGC TGACGGTGGA CGCGGCGCTC ACCCGCCTGA TGTTCCGTGG	300
TCAGTGTGTTG GCCGGTTATT CGTCAGGCC GGGGGGGGGT AAATACGTAT CTGTCGGTAG	360
CGGCGGGTT TGAGTGCACT GCGCTCATCT ACGACAGCTA CCATTACATC ACCATCCAGG	420
CCCCCAATGA GGGTCGGTG TGTCGTTCG AACATGGAGG GTGGTACGTT CCAAAGACAG	480
TGCTGAGCCT GCTGAGGCAG CGGAAGTGT AGGATGCTAG GGCTGATCTG AGGAAT	536

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

TGGGGCGCTG AGCTCCACCT TCTCGAnGGG ACTGAACGTC ATCCCACCTG GTACTGGAGC	60
GCTCGTTCAT TCAACAGGGT GTACCCGGGG TTAATAACGT TAAAGCGATT GGGTGTGCCG	120
AGCACGGATG TATGCGGTGT AAGCCAGGCG TGGGAACCGA GGGGGATGCG ATACTGCACC	180
ACGCCCTTCCC CAAAATTGGC ATATTGATAG TCCCAGGGGG CACAGCTCCA TTCAGTTCGT	240
ACCCCTCCGTT ATTTCTGTAA CGGATGTAGG TGAGGGGGAT GTACACGCGT GCTTCGACGC	300
CGGCCTTCAG GCCGGTGAGC AGGTGGGTGT AGGGGTCACC GCTTTGGTT TCGAGTTGA	360
CGGAATCCGGC AAAATCAAAA TGCCAGGACC GCAGCGCAGG CAGCACGCGC TTAC	414

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

GGCAACATAC ACCCGAGCAC CATCACTTAA CCCAGACGCT TCCCCACAT ACCCCTGCAA	60
TCCCTCGCCT GTAAACTGAG CGCGCACAGC CCCACGGGGC AAAACGCGCA CCCCCAGGGn	120
nACCCGTTCT CTGGCCCACA CGACAACCCC TCACCAAACC ACCTTCACCC CACAGATAAA	180
CGTGCCAAAG TAACGCTCAG ACCACATACT CTCGGCAATA CCCATGTAAG GAGCGTCAnA	240
AGTCACCCCC TGTTCCCCT GGGCGCTGAG CTCCACCTTC TCGAACGGAC TGAACGTCAT	300
CCCACCTGGT ACTGGAGCGC TCGTCATTC AACAGGGTGT ACGCGGGTT AATAACGTTA	360
AAAGCGATTG GTTGTGCCGA GCACGGATGT ATGCGGTGTA AGCCAnGCGT nGGAACCGAG	420
GGGGATTTCGA TTA	433

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

ACCTAGGGGA CGGCGCTGGG AGGAAAGAGT CCTGCCGGAA GnGCCCTGCG GCGGGTAGTA	60
GCTACCAGGA GAGGGTGACG CCGCACACGA TGCAGCCGAT TCCCTGGGTG AGGCACCTCGG	120
ACACCAAGCAG GTACGGGACA TCAGAGAGCA TACCCCTGTTTC CCAATCAAGG GAGAATACCG	180
TCTTCTCTAT GAGACTGGCT GAAATACCAAG CACGCAGCTG TGCACAGTAC TCCTTGGTTA	240
GATAGGTAGC TCCTACTGCT CCACCTGCAG CAGGGGCATT CAGGTGTGCA CGGTTGGTAG	300
AGGCATGGAC CGTAACGCTT GGCTTCACCC AGCCGTAATC CTGCACCGGG ATGCGATACT	360
AACACCACGC CTTCCCCACC ACCGGTGGAC GGATATACTC CTTTCCTGA ATGCC	415

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

1105

TCGTTGGTAA GTCTCGCTAC CAACAGGGCG CTGCCCTACT ATACGACAGC CGTGTGAAG	60
CAAGCTGTT CAGGAAAATA TACGGAGGAT CAACGCTGTG GTGCCAGCAA AAAGCGCAA	120
CGCTCACCTC TTCCCAGGAA CTGGAAAAGG CAGTGTATTG GTTGTTCGTT CCCACGTTG	180
AAAACCTGGT GTTGGGTGCA GGCGCGCTGC TGGCTTTTG GGATATGCAT CAGATTGCCG	240
TGGACGCGCT GTTTACGGCG CAGTGGAAAGT GGCTGTCTTC TGGCATATAC TTTGCCACAG	300
CACCGGCAAA CGTTTTGGC ACCAGGGTGT TAGATAACAC CATCGCAAGC TGTGGCGACT	360
TTGCCGGATT CCTTAAGCTC GAAACTAAGA GCGGTGACCC CTACACCCAC CTGCTCACCG	420
GCCTGGACGC CGGCGTTGAA ACACGCGTGT ACATCCCCCT CACCTATGCG CTATACAAAA	480
ATAACGGGGG GACGGCTGTG CGTGGCATTC AGGAAAAGGA GTATATCCGT CCACCGGTGG	540
TGGGGAAGGC GTGGGTAGC TATCGCATCC CGGTGCAGGA TTACGGCTGG GTGAAGCCAA	600
GCGTTACGGT CCATGCCCT ACCAACCGTG CACACCTGAA TGCCCTGCT GCA	653

(2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA	60
CCAAGTCATT CTGAGAATAG TGTATGCnGC GnCCnAnTnG CTCTnGCnCG GCGTCAATAC	120
GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT CATCATGGA AAACGTTCTT	180
CGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC CAGTTCGATG TAACCCACTC	240
GTGCACCCAA CTGATCTTCA GCATCTTTA CTTTCACCAG CGTTCTGGG TGAGAAAAAA	300
CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA	360
TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG TTATTGTCTC ATGAGCCACG	420
TTACGTGCTT CGnTTTTCTC CCGCTCACGC TTATCAn	457

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

TGATGCCGCA TAGTTAACGCC AGCCCCGACA CCCGCCAACA CCCGCTGACG CGCCCTGACG	60
GGCTTGTCTG CTCCCGGCAT CCGCTTACAG ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT	120
GTGTCAGAGG TTTTCACCCT CATCACCGAA ACGCGCGAGA CGAAAGGGCC TCGTGATACG	180
CCTATTTTA TAGGTTAACG TCATGATAAT AATGGTTTCT TAGACGTCAG GTGGCACTTT	240
TCGGGAAAT GTGCGCGAA CCCCTATTTG TTTATTTTC TAAATACATT CAAATATGTA	300
TCCGCTCATG AGACAATAAC CCTGATAAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT	360
GAGTATCAAC ATTTCCGTGT CGCCCTATTC CCTTCGAAAT ATCTGTGAGC GGAAAnTCTGC	420
GTGTTTACTC ACCTGGCAGC GACTAACGCG GCAACACCCA AGGACGAGCA GAAGATGTGC	480
CGGGCAC	487

(2) INFORMATION FOR SEQ ID NO: 675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

ATTCCTGAGAA TAGTGTATGC nGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAAA	60
TACCGCGCCA CATAGCAGAA CTTTAAAAGT GTACGCTCCT ATGATTAGAC GTTCCATCGT	120
CTTCTGGTTA AAGAGACTGG AGGTGCCCTT GTGATCGCG TGCAAnGTGCT CAATCGTCTT	180
GAATATCACG TCAAGGGAGT GGAGCGGnTT TGGATCGCGG TAAGTTAGTG AGGAAAATAT	240
GCCATGTACT GGATCTGGCA GGGTGAATGC ACCGTAAGCA CCACCTATCG TTCGAATTTT	300
TTCCCAAAAn GGGnTCAGTA CTTAGATATC GGGGnAAACA CCTGGCTCTA CCCCAGCGTCT	360
CTCCAAAGGA AGCCGTGGGA TGTGCAAnGG ACAGCGCTGC AAAACCCACT TGCACAGGGn	420
TGGAAGCAGC GTTCACATAT TGCGGGTGCG CATGTGCTGC AGGGCTCTTG AAAGAGCA	478

(2) INFORMATION FOR SEQ ID NO: 676:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

AACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAnAATTA TGCAGTGCTG	60
CCATAACCAT GAGTGATTAC AGACCCGTCA CTGCTTCTCA CACACGCATC GGCAGTGCTC	120
TGCCACGCT TTCCTGCATG ATTACGCGGT GAACAnGCAG CATTGGTAA AATTACCGAA	180
TCATTCCTAG GACGGGGCCC AATACCCCTCG GTGCGAAACA AATCCAGACA ATCGCGCACC	240
ACACGCAAnGA AGCGTGCAGT ACTCTCTCTG TCCCCAGnGT GCATAGGACT GAGCCTACCA	300
TAAACTGCGT ACATGACGGT ACCCGATCCT TGACATCTGT CAATAGACAC TACACGAGCT	360
CTGCCCGCGG CACAGTGGGA ACGAACCGAC GCGTACGCAC CTGGnAGCCG TTGGGGTAAG	420
TCTGTTAAAA nCTATAACCTG TGG	443

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

CTGCTACAGA CGTGGGGCAT AAGAAAAACG GAGCGAATGG CGACATAGGC GCAGATGCGT	60
TGTTGACGTT GGGGTATCGT TGGTTCTCGG CGGGAGGATA TTTCGCATCG AAGGCCAGCA	120
ATGTATTCCGG GGGAGTATTT CTCAACATGG CCATGCGAGA GCACGACTGT GCTGCCCTATA	180
TTAAGCTCGA AACCAAGGGG TCTGATCCTG ATACTTCTTT CCTTGAGGGT CTTGATTTGG	240
GTGTTGATGT GCGTACGTAC ATGCCGTCC ATTGGAACGC CTTCACCCAA GCCCGAGCCC	300
TACCCGGAGC CGACATCCAC TTCCCGGTGT ATGGAAAAGT CTGGGGTTCG TATCGTCATG	360
ATATGGGTGA GTATGGTTGG GTTAAAGTGT ATGCAAACCTT GTACGGCGGT ACGAACAAAA	420
AAGCTGCTGC TGCAGCCCT GCTGCTCCTA CGAATGGAAn GGCAGAATAT GTGGGTATAC	480
GAAnTGTGGGG TATGGTCATC CGTTAGAGAA GTGGAGAT	518

(2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

CGAAACGGTA	GCCGTCGCGT	CTATCCCCA	GTGCGCGCTA	AAATAGTGCT	GTACCCCCAG	60
CTGCACCGGC	ACCGCATAGT	TCTGACAGAC	CCCTTTAATA	CGCCGACTCT	TCGGTGTATGG	120
CGCCTACCTC	CTTGGCAGTG	CACGTTAGCA	CGCCAAGCAA	TGAACGTGGG	CGGTGCCAGT	180
TACCGGCTGA	ATAAGACGAG	CTGCTCGGCT	GCAGTAAGCC	CTGCCAAGA	ACCGAAAGAA	240
AGTGCTGGCT	ATCGTAGATG	AGCGCGGTGC	ACTCAAAACC	CGCCGCTACC	GACAGATGCG	300
TACTACCTTC	CCCCGGTCTG	AACGAATAAC	CGGGCCAAAC	ACCGGGCCGC	AGAACATTAA	360
ACCGGTGAGT	GCCGCGTTCC	ACCG				384

(2) INFORMATION FOR SEQ ID NO: 679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

CTGACGTCTA	AGAAACCATT	ATTATCATGA	CATTAACCTA	TAAAAATAGG	CGTATCACGA	60
GGCCCTTTCG	TCTCGCGCGT	TTCGGTGATG	ACGGTAAAAA	CCTCTGACAC	ATGCAGCTCC	120
CGGAGACGGT	CACAGCTTGT	CTGTAAGCGG	ATGCCGGGAA	GGTAAATACT	CCATCTCCGT	180
GTCATCGGGA	TCCCCACTTA	CCTCCCTCTGC	ATCGGTGCGC	TTAATACACA	AGCCCCACAG	240
GTCAGGACCG	CCACGTGCGT	CCCCATACGC	CCCCAGCTTG	GGAGAGACAG	AAATACGCGC	300
GGCCACGCAC	GGCAACGCAC	ACCCGAGTAG	CACCACTTTA	CCCAGACATT	TTCTCCACAT	360
ACCTTCACTC	CTCCCCGCAA	TTCTTCGACA	GGACCCGTTTC	CTCCCCGGCGC	CTCCCCCTAGG	420
TGCGGAAGAC	CGGGCCAACG	CGAACGTAT	ACGGGATGCG	GAACTTAGCC	AGCTTGGTGT	480
CAATGCCAAA	CGAAACGGTA	GCCGTCGCGT	CTATC			515

(2) INFORMATION FOR SEQ ID NO: 680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

CCCCCTGACGA	GCATCACAAA	AATCGACGCT	CAAGTCAGAG	GTGGCGAAC	CCGACAGGAC	60
TATAAAAGATA	CCAGGCCTTT	CCCCCTGGAA	GCTCCCTCGT	GCGCTCTCCT	GTTCGGACCC	120
TGCCGCTTAC	CGGATACCTG	TCCGCCCTTC	TCCCTTCGGG	AAGCGTGGCG	CTTTCTCATA	180
GCTCACGCTG	TAGGTACAGT	AGGCGGAAT	AAAAATTCAA	TTAAGATTAT	TGGTGAGGCG	240
ACGGATAATA	ACGCGCAGGC	TTACTTTGCC	TACGATAGCA	AGAAGTCTGG	TGGTTTTACT	300
ATTTCTCATT	TGCGTTTTGG	AAAGCAGAAG	ATCCGTAAGC	CCTACCTTCA	TTACGCAGGC	360
GGATTTTGTA	GCGTGTCAATA	AGTTTACGTA	CCTTGAAACC	TTTGACATGC	TCAAAACGCT	420
CAAGCGTGG	GGGACCTTTT	TGCTGAATGC	GCCGTACAGT	GAGCATGAGG	TGTGGCATCA	480
CATAACCCATA	GAAGTCCAGC	GTCAGATCAT	TGAAA			515

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

TGGCAGTTTC	TGTGGTCAAC	GCGCTGTCGT	TGTGGGTAGA	AGTGACAGTG	TATCGTGATG	60
GTGCTGAGTA	TTATCAGAAG	TTTAATGTGG	GGATGCCGCT	TGCTCCAGTA	GAGAAGCGGG	120
GAGTGTGCGGA	AAAACGTGGG	CACTATTATC	CGCTGGCAGG	CGGACCCATC	CATTTTCAAA	180
GAAACGGTGG	CCTATGATTT	TGACGTACTC	CTGACGCGTT	TGCGTGAAC	TGCTTTTTTG	240
AATACCCATT	GGGCTTGAAG	ACCGTCTAGA	GGGTGTCATC	GATTTAATT	CGCTCAAAGC	300
CCTTTATTTC	GAGGGAGAAA	GTGGCGCGA	CGTGCCTGAG	GCGCCCATTC	CCGAACAGTA	360
TCAGGCAGAT	GTGAAAAGT	ACCGGGATGA	ACTCATCGAT	GCGGCGTCTT	GTTCCTGAC	420
GAGCTTGCTG	AGGCCTACCT	TGAAGGAAC	GAGACCGATC	AATTGATTG	AGCGGCATAC	480
GTGCGGGCAn	CATTGCAGAA	AAGTTTGThC	CGGTTTTTG	CGGTTCTGCG	TACAAAAATA	540
AAGTATTCA	CCACTTTGGA	CGCT				564

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1110

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

ACACAGCCCA GCTTGGAGCG AACGACCTAC ACCGAACCTGA GATACCTACA GCGTGACTAT	60
GAGAAAGCGC CACGCTTCCC GAAGAGnAAA GGC GGACAGG TATCCGGTAA GCGGCAGAGC	120
TGCTCTTAAC TGACTTTCGT GCTGC GTTGG AGGATGACTT TTCTACGCCA CGTGCTCTGA	180
GCGCCTTACA AAAATTGGTG CGTGATACCT CGGTGCCGCC ATCGCTGTGT GTTCGGCAC	240
TCCAGGTGGC GGATAACAGTG CTAGGGTTAG GCATAATACA GGAAGCGACC GCATCGCTAT	300
CTGCGCAGGT TCCTGCTGGC GATACGTTGC CGCAGCGTCC TTTACCGAGT GAGGAGTGGA	360
TTGGACAGTT GGTGCGTGCG CGTGCACATG CACCCAAACG CGTGATTTTC CCCGTGGCAG	420
ATGAGATCCG TC	432

(2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

TGnTAAC TCT GCCTTAAAT AAATAAATAA ATACATCTT TAAAAAATTG AATGGAAAAG	60
CTCAACATCA AAAATCCTT CCTGTGCATA TAAATAAGTG CAGGCAATAG GGGAGGGTGA	120
CATTATTCCT ACTTG TATAA AGAACTGTTT AGGCCGGCAC CGCGGCTCAC TAGGCTAAC	180
CTCCGCCTAG CGGCGCCGGC ACACCGGGTT CTAGTCCCGG TTGGGGCGCC GGATTCTGTC	240
CCGGTTGCC CTC TTCCAGG CCAGCTTCT GCTGTGGCCA GGGAGTGCAG TGGAGGATGG	300
CCCAGGTGCT TGGGCCCTGC ACCCCATGGG AGACCAGGAA AAGCACCTGG CTCCGGCTC	360
CTGGCTCC TG GCTCCTGCCA TCGGATCAGC ACGGTGCGCC GGCGCAGCG TGCCGGCCGC	420
GGCGGT CATT GGAGGGTGAA CCAACGGCAA AGGAAGCCCT TTCTCTCTGT CTCTCTCTCT	480
CACTGTCCAC TCTGCCTGTC AAAAATAAA AAATTAAAAA AAAAATGTT TAGTTTTTG	540
TTGCATTAGT CTCATAGTAT CTTACTGGAA AnGTGTTCCA GTGTCCTAAT GGnCATTCAG	600
GGGCTGAAC T GCCATGATG GTAAATTTT GGGATAATTG ATAAATAATG CAATTTTCT	660
TCTCTAGAAG AATGGnnTTT CTCCAACCCCC T	691

1111

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

TGCTGCAGTG	GTTAATGAGA	CGTAATCAAC	ATCATCATGG	CCTTGACAC	ACCATGGCAT	60
CACTTCCCTG	AGACAGTGCT	AGCCTGGTC	TTTAAGCATG	CTTTTAATCC	GACAGGTCAG	120
ACTTTATATA	AACTATCCCC	CCCCCCTTTT	TTTTTGACA	GGCAGAGTGG	ACAGTGAGAG	180
AGAGAGACAG	AGAGAAAGGT	CTTCCTTGTC	CGTTGGTTCA	CCCTCCAATG	GCCACCGCGG	240
CCAGCGCGCT	GTGGCCAGCG	CACCGCCTGA	ATCCGATGGC	AGGAGGCCAGG	AGCCAGGAGC	300
CAGGTGCTTT	TCCTGGTGTC	CCATGGGGTG	CAGGGCCCAA	GCACTTGGC	CATCCTCCAC	360
TGCACTCCCT	GGCCACACCA	GAGGGCTGGC	CTGGAAAGAGG	GGCAACCGGG	ACAGAAATCCG	420
GCGCCCTGAC	CGGGACTAGA	ACCCGGTGTG	CCGGCACCGC	TAGGCGGAGG	ATTAGCCTAG	480
TGAGCCGCGG	CGCCGGCCCC	GTTTTTCTT	TAATTTAGTG	CAAGGAACTC	AGGTTTATTG	540
TCAGAAATGG	AAATGATGGC	TGATAnCTGC	GTGCGT			576

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

CnGAGAGAAA	GGTnTTCCCTT	TGCCGTTGGT	TCACCCCTCCA	ATGGCCGCCG	CGGCCGGCGC	60
GCTGCGGCCG	GCGCACCGCG	CTGATCCGAT	GGCAGGAGCC	AGGAGCCAGG	TGCTTTTCCT	120
GGTCTCCCAC	GGGGTGCAGG	GCCCAAGCAC	CTGGGCCATC	CTCCACTGCA	CTCCCTGGCC	180
ACAGCAGAGG	GCTGGCCTGG	AAGAGGGCA	ACCGGGACAG	AATCCGGCGC	CCCGACCGGG	240
ACTAGAACCC	GGTGTGCCGG	CGCCGCTAGG	GGGAGGATTA	GCCTAGTGAG	CCACGGCGCC	300
GGCCCATAAA	ATAAAATCTTT	AAAAACAGTT	TATTTTAAA	AAAGGTGGCT	TTAATTTCT	360
TTTATTTTG	GCAAAGCTAT	GATTGTAAGA	GTGTTTGAAA	AGGTAACACA	TCTCCTTTTC	420

1112

CTTAGCCACA CTTTTAAACC TTTTGCACAG AGGTTAGTTT TTGTTCATCT CATAGTTAAT	480
GACATGAAAT AGAGGGTGGC AAACCTTTTC TCCAAAGGGC CAGATGGTAA ATAGTTGGG	540
TCTTTGGGC CACATGTGGT CTCTGTTGTG TATTGTT	578

(2) INFORMATION FOR SEQ ID NO: 686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

TACGCCTATT TTTATAGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA	60
CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA	120
TGTATCCGCT CATGCAATAA TGAATACGCT CAGGAGACAG CCGCTAACCC AAATTGCGCG	180
CAAnGGGTAA TGAAGGTGAG GGATATATAT CTTGGTGTG AGTTTAGTCC AGAAAATCCT	240
GCGCAGACAT CTGCCCTTC TTTTCCTCAG AGTAACGTGC TGCAGTATT TGTACAGGGT	300
GGCAGTATGT AAGTATACGA CCGAGTGGAA CAGAACAAAA AATAAAAGTGT TATATCATCC	360
ACCCCTCTGGA CCGTCATACC TCGATAGAAG AAGCAGAACAA GGCGGGGCAA CAGGTTATCA	420
CCGCnTTGAA CCAGAGGnGG GGACATATCT GCCATGGTAT A	461

(2) INFORMATION FOR SEQ ID NO: 687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

CCCTGATAAG ATTTTAGACT CCTACTCTCC TTCGCACGAG AGTCCGGTCA GTCACCACCG	60
TGCGCGTATA TTCGGGGGAG TATTCTCAC CAATAACATG CTGCAGCACG ACTGCGCATC	120
AGACGTGGGG CATAAGAAAG AGAATGCAGC GAACGTCAAT GGCACCGTGA GCGCCGGCAC	180
GCGGGGCATT GCATCCGAAG ATGGTAnCGC CGGAAACCTC AAGCATGGAA AGCCGCGCGC	240
AAAAGACGCA ATTCCACCCCT GACGGGGAGG GCAAGTCAAA CACGGCGGCC GCCCCAGCAG	300
GAAGAAACCA CAGCGCCCGC TTTGCACGCT ATGCTCCTGC TACGAATGGA AGGCAGAATA	360

1113

TTGTGGGTAT TACGAGTGTG GGGTAGTGGT CAATCCGTTA GAGAAGGTGG AGATTCGGCT	420
GAAGCTGGGA GCAAnGCAA GCTACAAGAG AACAGCAATG TAGTGATAnA GAAAAACGTG	480
ACGGAGCGTT TGCAATTCTGT AAGGGCAT	508

(2) INFORMATION FOR SEQ ID NO: 688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

ACTTCAAGAA CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG	60
CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTTACCGG	120
ATAAGGCGCA CGGGTCCGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA	180
CGACCTACAC CGAACTGAGA TACCTACAGC GTGAGTATGA GAAAGCGCCA CGCTTCCCAG	240
AGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAAGGTCCG ACAAGAGAG TTCGCGTAAC	300
GTTTCACATG GAAAnAGCAGC GCTTCCCGAA GCCAACACAC GTTGCAAAAG GCGGCACACCG	360
AATTTCAAG CACTGGGCA nCTGGnCAGA GGGCACGGAT CGCTAnCTGC TCTCCGATTC	420
AAGCCGGCGC AAAGTG	436

(2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

TGCAGGTAAC ATCTCTAGGA CCTCACTATC ATTGCTTTAT ATCACTATTT TATTTAATAG	60
GCTTTTTTT TGTTTTTGAC AGGCAGAGTG CACAGTGAGA GAGAGAGAGA GAGAGAGAGA	120
GAAAGGTCTT CCTTTGCCGT TGGTCACCC TCCAATGGCC GCTGTGGCCG GCACACGGCA	180
CTGATCCGAA GCCAGGAGCC AGGTGCTTCT CCTGGTCTCC CATGGGTGC AGGGCCAAG	240
CACTTGGGCC ATCCTCCACT GCACTCCCGG GCCACAGCAG AGAGCTGGCC TGGAAAGAGGG	300
GCAACTGGGA CAGGCTCCGG CGCCCCGACC GGGGCTAGAA CCCGGTGTGC TGGTGCCGCA	360

1114

GTGGAGGATT AGCCTAGTGA GCCACGGCGC CGGCCTTCAGA TAGGCTTTA ACCCAAGCCT	420
GGCACCCCAA GATTCAGAA GCTCCAAGAG GACTTGCTG TTTACATTAG CACAGGTTT	480
ATTATAAAAAn nGCTGATTG GGCCCTCTTC TCTAATTAAT AGTACTTTA GnCACATT	540
TAAGATGTTT ATGAAGATGT TACTGCATTG CTGCATTAT GATTACnGTA AGACACCTCA	600
AAG	603

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

ATAATTCTAA AATTCTGTC ATTTCAGGGT TGACACGAGG CTGGTGCCGT GGCTCAATAG	60
GCTAATCCTC CACCTAGCGG CGCCGGCACA CCGGGTTCTA GTCCCCGTCG GGGGCCGGGA	120
TTCTGTCCCG TTGCCCCCTC TTCCAGGCCA GCTCTCTGCT GTGGCCAGGG AGTGCAGTGG	180
AGGATGGCCC AGGTGCTTGG GCCCTGCACC CCATGGGAGA CCAGGAGAAC CACCTGGCTC	240
CTGCCCTCGG ATnAGCnGG TCGTGACCT GCAGCGGCC GGCTGCGGA GCCATTGGAG	300
GGTGAACCAA TGGCAAAGGA AGACCTTCT CTCTGTCTCT CTCTCTCACT GTCCACTCTG	360
CCTGTAAAAA AAAAAAAA AATACTGTGT CTTGGGGCTG GCATGTGGTG CTGAAAATCC	420
CATATGGGCG CTGGTTCGAC TCCCAGCTGC TCCACTTCCA TCCAnCTCTC TTCTATGGCC	480
TCAGAAAGCA GCAGAAGATG GCCCAAGTCC TTGGGGCCCT GCAACCATGT G	531

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

GAGCAAGGCA AGACTACAAG AGAACAGCAA TGTAGTGATA GAGAAGAACG TGACGGAGCG	60
TTGGCAATTG GTAGGGGCAT GTCGTTGAT TTGGTAGAGA ACGGCATGCC CGTCTATTAC	120
TTCGCAGCCC GAGCCCAACT CCCAGCCGTA GCCCCAGCCA ATGACATCTT ATGGGACGCA	180

1115

GGCTTACATG CCCgTCCATT GGAACGCCTT CACCCAAGCC CGAGCCCTGC CCGGAGCCCC	240
AkTCCCAGCC ATCTACTTCC CGGTTGTAGT TACAATTCCA CGCTTCTGG CGACTATGCC	300
CGAGCCGCAG CCGCAGCCGG GGCTGGAGTC GACATCAACT TCCC GTGTGA TG GGGGTGTC	360
TTGCACGCAT CGCAGGCTAG TAATGTATTT CAGGGTGTCT TTCTCACCGA TACCACACCC	420
ATGCGGACGC ACGACATACC CCGCAGTCCC CTCGTGGGGC ATAAGAAAAA CGCAGCTCCC	480
GATGGCATAG GCGCCTCACG CGCGTGCTGC CCAGCGCGCG AGAACGAACC CT TT AAAAAG	540
GGTTCGACAA ACAGCCGTGG GGGGGGGTA GAATGGAGTA GGTCTCGAC GAGACGCGTA	600
AGAGGATCGG CGTTGGAGCG GGGTATGAA	629

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

GATAACCAAT AAATTCAGTG TCTGGATTTC CTCGGGAGAG TTTCCATTGG ATTCTGTGG	60
CTGTATCATA CCTTCTTAG TGTGTGTCCC ATTTTTTGTG TTGTTGCTG TTGTTGGTAA	120
TTGGATATAT ATATTTTTT TTTGACAGGC AGAGTGGACA GTGAGAGAGA GAGACAGAGA	180
GAAAGGTCTT CCTTTCGGT TGGTCACCC TCCAATGGCC GCCGCGGCCG GCACGCTGCC	240
GCCGGTGCAC CGCGCTGATC CAAAGGCAGG AGCCAGGTGC TTCTCCTGGT CTCCCATGGG	300
GTGCAGGGCC CAAGCACCTG GCCCATCCTC CACTGTACTC CCGGGCCACA GCAGAGAGCT	360
GGCCTGGAAG AGGGCAACC GGGACAGAAT CCGGCGCCCT GACTGGACT AGAACCTGGT	420
GTGCCGGCGC CGTGGCACTG GCCGTAATT GGATATTGCA AATAATTGAT ATTTGGAAC	480
TTTAGGAAGC AGATGCTCTT AATGAACAAG GTTGCTGTTG TTGGCTCAA TGTTTAATGC	540
C	541

(2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

AACGCCTGGT ATCTTTATAG TCCTGTCGGG TTTGCCACC TCTGACTTGA GCGTCGATT	60
TTGTGATGCT CGTCAGGGGG CGGGACTAAT GGAAAAACGC CAGCAACGCG GCCTTTTAC	120
GGTnCCTGGC CTTTGCTGG CCTTTGCTC ACATGTTCTT TCCTGCGTTA TCCCCTGATT	180
CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTGCCGC AGCCGAACGA	240
CCGAGCGCAn GGTTCAAGTGA GCGAGCCGCG CGTGTTCATA ATAAGGTGGG GCTAGAGGAG	300
GATCCTTCTA ACTTCTTGCT TATGCACGCG ATGGGTCTA ACGTGGCTGG TGTCATTGGG	360
ACCGCGATAC CGCAGGGTGT TCATCTCGC CTACGGAGGG TAGGGAGGAA GAGTAACCGC	420
GGGGTTTTGC CGCTTAGGTA ACCTTCCTC CGTGCAGGGG CAnAnCCTCT CanGTGGGCT	480
AAGGGGnTTT TGCAGACGAA GCGGG	505

(2) INFORMATION FOR SEQ ID NO: 694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

AAGAGATTTT TTTTGACAG GCAGAGTGGA CAGTGAGAGA GAGAGAGAGA GACACAGAGA	60
AAGGTCTTCC TTTTGCCGTT GGTTCACCCCT CCAATGGCCG CTGCGGCCGG CGCACTGCAG	120
CCAGCGCATC GCCTGAATCC AAAGCCAGGA GCCAGGTGCT TTTCTGGTC TCCCCTGGGG	180
TGCAGGGCCC AAGCACTTGG GCCATCCTCC ACTGCACTCC CTGGCCACAG CAGAGAGCTG	240
GCCTGGAAGA GGGGCAACCG GGACAGAACATC CAGCAnCCCA ACTGGGACTA GAACCTGGTG	300
TGCCAnCGCC GCAAGGGGAG GGATTAGCCT ATTGAGCCAA AnCGCTTGGC CAGCAAAGAG	360
ATTTGGATAT TTCATTTCCA TTACAGCCAA GGTTTGGTCA GGTCAACTAG GAGCCAGGAA	420
TCTTATCCAG GTCTCCCCAC GTGGGTGACA GGGACCCAAA TATTCAAGCTT TCATCGTTG	480
CTCTAnGCTA ATGnATTAAC ATGAAAGCTA AATTGGATGT TGTTAA	526

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

GGTGCAGCGG CTCAGTAGGC TAATCCTCTA CCTTGCGGCG CCGGCACATC GGGTTCTAGT	60
CCCGGTCAGG GCGCCGGATT CTGTCCCAGT TGCCCCCTCTT CCAGGCCAGC TCTCTGCTGT	120
GGCCCGGAAG TGAAGTGGAG GATGGCCAA GAACCTGGGC CCTGCACCCC ATGAGAAGAC	180
CAGGAGAAC ACCTGGCTCC TGCCATCGGA TCAGCGCGGT GCACCGGCCG CGCGCGCCA	240
GCCGTGGCGG CCATTGGAGA GTGAACCAAC TGCAAAAGGA AGACCTTTCT CTCTGTCTCT	300
CTCTCTCACT GTCCACACTG CCTGTCCAAA AAAAAAAA AAAGAnAGA AGAAAAAAA	360
AAAACACTTT GATGTAAATA TGTTCTTAA AAAAAAGTAT GCTCAATTTC TATTATATTA	420
TTAAnAGTAT TCTAAAAACn ATATAAAGGG GT	452

(2) INFORMATION FOR SEQ ID NO: 696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTnACCGG	60
ATAnChCGCA CGGnTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA	120
CGACCTACAC CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCG	180
AAGAGAAAGG CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGGGA	240
AATAAAGGCC ATGCGCGTGA AGTGCCTTTC TCCAAGCGAG CTTATCAGTG CGCTCAGCGG	300
GGGTAATCAG CAGAAAGTCA TTATTGGAAA TGGCTCGAAC GCGATCCCGA CGTCCTCTTG	360
CTTGATGAGC CGACCAGGGG GATCGACGTG GGTGCGAAAT ATGAAATTAA TCAGCTCATC	420
ATTCGTATGG CGCGTGAGGG AAAGACAATC ATGTGGTTTC TAGTGAAATG CCTGAAATTc	480
TT	482

(2) INFORMATION FOR SEQ ID NO: 697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

GTTGGTTCAC CCTCCAGTGG CCGCCGCGGC CAGTGCCTG CGGCCAGCGC ACCACGCTGA	60
TCCGATGGCA AGAGCCAGGT ACTTCTCCTG GTCTCCCCTG AGGTGCAGGG CCCAAGCACT	120
TGGGCCATCC TCCACTGCAC TCCCGGGCCA CAGCAGAGAG CTGGCCTGGA AGAGGGGCAA	180
CCGGGACAGA ATCCGGCTCC CCGACCGGGA CTAGAACCCG GTGTGCCGGC GCGGCAAGGT	240
GGAGGGATTAG CCTAGTGAGC CGTGGCGCCG GCCGCGATTG TGTTTAAACA TGCCTGCACA	300
TCTGCCTGAA GACAGTTCAA TTCGTATCTG CCTTGAGTCG CTGAGAATCT TTCTTCCCAG	360
TCTGTTATTT ATCATCTGTC ATAAGCATGA CCTGAAATGC TGATTGGAAT CANTCATCTG	420
ATAAGATCCT AACATCTCCT TCTCTGAAAT TTTCTATAA TTTCTCTGGA ATAAATTGTG	480
AATATACAAG GCTTACTAAT AACATTCCT TATCAGATAT TAATAACATT GTTCGTCTGC	540
TTTTGGCTCC CTTTGTCTCT CTATTGAGGG CCTTATTGCA	580

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

CGCTGCGGCT CACTTGGCTA GTCCTCTGCC TGCGGCGCCT GCACCCCTGGG TTCTAGTCCC	60
GGTCGGGGCG CTGGATTCTG TCCCGGTTGC CCCTCTTCCA GTCCAGCTCT CTGCTGTGGC	120
CTGGGAAGGC AGTGGAGGAT GGCCCAAGTG CTTGGGCCCT GCACCTGCAT GGGAGACCAC	180
GAGGAAGCAC CTGGCTCCTG CCTTCGAATC GGCGCACGTG CTGGCCGCAG TGCGCCACCG	240
TAGCAGCCAT TTGGGGAGTG AACCAATGAA AGGAAGACCT TTCTCTCTGT CTAACTCTGC	300
CTGTCAAAAA AAAAAAAAAA AAAAAAAAAA GGATGATAGA CTATGAGCTG TGACTATTTT	360
AAAATTATT GTATATGAGT GAAATAGACA TCTTTTCATT TATTACTGCT TATGGCCTTG	420
CCTATATTCC TGCAGGAACTA TGGTGTCCCC ACTTGTTGAA CTCTTTATTT AGTGGAGCAC	480
TAAAGATTTG ACTATTTGTA ATGnATGTTA AAAATATGTT ATCTTGGGGC CGGAGCTGTG	540
GCACAGCAGA TTAATGCCCTT GGCCTGAAG	569

(2) INFORMATION FOR SEQ ID NO: 699:

1119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

TGTAAATTAT GTGTTGAGAG GGTTACCTTT TTTTTTTTTC AAAATAAATT GTGCCACTA	60
GGAAAAGAGG GCAATGTATT TTGTTAAATT TGGTTGCTAA GAAATGATGT GTTAGTCACG	120
TGAATTCTCT CAAACATCAG ATACTTTCT GCTTCAAGGC CTTTATTTTT GTAGGTACAT	180
TGCCTAAAAA AATCTTTTTT TTTTTTTTTT TTTTTTTTTT TTGACAGGCA GAGTGGACAG	240
TGAGAGAGAG AGACAGAGAG AGAAAGGTCT TCCTTGCCG TTGGTCACC CTCCAATGGC	300
CGCCGCTGCA GCCGGCGCAC CGTGCTGATC CGATGGCAGG AGCCAGGAGC CAGGTGCTTT	360
TCCTGGTCTC CCATGGGGTG CAGGGCCCAA GCACCTGGGC CATCCTCCAC TGCACTCCCT	420
G	421

(2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

CCCTTGGGTA AATTCCCAGG ACTGAGAGGC CTGGGTCTATA TGATAGGTCT ATATTAGATT	60
TATTTTAAAT ATTTATTTAT TTGAAAGAGT AACACAGAGA GAGGAGAGGC AGAGAAAGAG	120
GGATCTTCCA TGCAATGGTT CACTCCTGAG TTGGCCGCAA CAGCCGGAGC TGTGCCAATC	180
TGAAGCCAGG AGCCAGGAGC TTCCTCTGGG TCTCTGACGT GGATGCAGGG GCCCAGGGAC	240
TTGGGCCATC TTCTACTGCT TTCCCAGGCC ATACTAGAGA GCTGGATAGG AAGTGGAGGA	300
GCCAGGACTA GAACCAGCGC CCATAAGGGA TGCTGGCGCT TCAGGCCAGG GCATTAACCC	360
ACTGnCGCTA CAGCGCCGGC CCTGGTCTAT ATTAGATTTT GAGATATCTC TATACTGTTG	420
TCCACAGTGG GCTTTACCAAG TTTACATTCC CACCAAGTAGT GGATTAGGGT ACCTTTCCCC	480
CCACATCCTC GCCAGCATTT GTTTGTGAT TTCTGTATGA AAGTCATTCT AACTGGGGTG	540
AGGTGAAACC TCATTGTGGT TTTTGATTTG CATTCCCTG GATTGCTAGT GATCCTGAGC	600

1120

ATTTTTTAAT GTATCTGTAG CCATTTGGAT TTCCTCTTTC GAGAAATGTC TTTTTAAGTC	660
CTTGTCCCCAT TTCTTGACTG GGGCTGTTG TTTTGTGAT G	701

(2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

CCACCGTCTA CCAGnGTGGT ATCTGTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA	60
AGTAACGGC TTCAGCAGAG CGCAGATAACC AAATACTGTT CTTCTAGTGT AGCTTGTGTA	120
TTAAGGCGAn CGATGCAGAn GAGGTAAGTG GGGATCCCGA TGACACGGAG ATGGACTATT	180
TACCTCCCCG nTATGCGCCG GAGACGCCGC TGGnGGGACT CGATGTGGCG TTCCGTGCGG	240
ACAATGG	247

(2) INFORMATION FOR SEQ ID NO: 702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

AAGTCACTTG CTGCTGCTTT CTTAATAGCA TTAAGAGGGA GATGGATCAG AATTGGAGCA	60
ACTGGGACTC CAACCAACAC CCATATGGGA TGCTGGTGT GCAGGCAGCA GCCTTAACCA	120
TTATGTCACA TCACCATCCC CAAAGGGAAC TTTATAGCAG TAAATGCTAT AGAAAACAAA	180
ACCCGGGGCC ACCACTGTGG CATAGCAGGT AAAGCCGCCG CCTGCAGTGC CAGCATCCCA	240
TATGGGCACC AGTCGAGTG CCAGCCACTC CACTTCAATC CAGCTCTCTG CTGTGGCCTG	300
GGAAAGCAGT AGAAGATGGT CCAAGTGCTT GGGGCCCTGC ACCCACGTGG GAGACACAGA	360
AGAAGCTCCT GGCTCCTGGC TTCGGATCTG TGTAGCTCCA GGTATTGTGG TCAACTGGGG	420
AGTGAACCAG CGGATGAAAG ACCTCTCTCT CTCTCTCTCT CTGCCTCTTC TTCTCTCTCT	480
GTGTAACCTGG ACTTTCAAAT AAATAAAAT AAATCTTATA AAAAnAAAAA ACACAAAGAT	540
CTCAAATCAG CAACCTTAGT TTTGTACAAT AAA	573

1121

(2) INFORMATION FOR SEQ ID NO: 703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

CCTCGTGC	G	TCTCCTGTT	C	GACCCCTGCC	GCTTACCGGA	TACCTGTCCG	CCTTTCTCCC	60
TTCGGGAAGC	G	TGCGCCTTT	C	TCATAGCTC	ACGCTGTAGG	TnCGGCTCCC	TCnCCTTTGC	120
TGATGAAACA	G	AAAAGCTTG	C	CCTGGCTCGC	GCGCCAAGGT	TTCGTGACGG	TACATTGCA	180
TCGCTGCGCT	A	ACGCACAGG	A	AAGTTGTTGC	ACTCCGATCT	GAGATTATG	GCACGCGCGA	240
GCTGTTGnCT	T	TACAnGATCG	A	ATGGCCTGGT	AGTAAAGAGT	ACCGATCTTG	GACTTCCAGG	300
ACGTA								305

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

AnATCGACGC	G	GGAACTGGCC	G	CACGGCGG	CGCACCCACGC	TGATCCGAAA	CCAGGAGCCA	60
GGTGCTTCCT	C	CCTGGTCTCC	C	ATGCGGGTG	CAGGGCCCAA	GCACTGGGC	CATCCTCCAC	120
TGCACTCCCG	G	GGCCACAGCA	G	GAGAGCTGGA	CTGGAAGAGG	AGCAGCCAGG	ACAGAATCCG	180
GCGCCCCAAC	C	CGGGACTAGA	A	ACCCAGAGTG	CCGGCGCCAC	AGGCAGAGGA	TTAGCCTAGT	240
GAACACGGCG	C	CCGGTCCGGG	G	CTTTTATTTC	GCTTGAGGAC	CTCTATTGGT	CATTATTGGT	300
CACTCCGTCT	C	CCTCCACTGC	C	CCTGTCTGAG	CTTTGTCTGC	TCCTGTCTCT	TTTAGGCCTA	360
GAGGTGACTT	T	TTCACCCCTGG	G	GTGCGCTCTG	ACACCCCTTC	CTGCTnCTCC	TTCAACCCCA	420
AGCACAGCTT	T	TGCAAATCCA	T	TCTTCTATGA	TGTGGCCAGA	TnGGGTGTGG	TATCAGCTCT	480
TGCCGGGGCT								490

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs

1122

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

GCTCTGGCCC AGAAGTACTG TGGAGGATGG CCCAAGTGCT TGGGCCCTGC ACCCACATGG	60
GAGACCAGGA GAAGCACCTG GCTCCTGGTT TCGGATCAGC ATGGTGTGCC AGCCACAGCG	120
CGCCACCACA GCCACCAGTG GAGGGTGAAC CAACGGTAAA GGAAGACCTT CCTCTCCGTC	180
TCTGTCTCTC TCACTGTCCA CTCTGCCTGT AAAAAAAAAGAAGTAAAC ATGAAACATG	240
TCACCACCAA ATTCACTAAC ATTCAAGGTAG GATCATTATC CAACCAACAA AATGACAGGT	300
CTTAATTTTT ATTTCTCAGT ACTAACCTTG AATGTAAATG GATTAAATTC ACCAACCAAA	360
AGACTTAGAG TGGCTGAATG GATTAAGAAC CATGACCCCCA TTATATGCTG CCTACAAGAC	420
ACTCATTCCA CAAACAAAAG TACACACAGA CTTAAATTGA AGGGTTGGGA AAACATATAC	480
CAAGCAAATG GAAACCCAAA ATGAGCAGGC ATAGCTATCA CAATATTCAA TGAAACAGAC	540
TATAAATCAA AAGCTATCAA AAAGATTAAG AAGGnCATTA TATTTGATA AAAG	594

(2) INFORMATION FOR SEQ ID NO: 706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

ATATAAGTGA GATCATGTAG TACTGTCTT TCTGGACTGG TTTATTTGTA ATTTCATGAT	60
CTCCAAGTCC ATCCATGTCA TTGCAAATGA CAGGAATTCA TTCTTCATAA GGCTGAATAG	120
TATTCCATTG TGTTATGTAC CACGATTCCCT TTATCCATTG AGGGTTTATG GACACCTAGG	180
TTGATTCCAC ATCTTGGCTA TTGTGAATAG TGCTGCAGCA AACGTGCGGC TTTAGATATC	240
TCTTCAACAT ACTTATTTAA TTTCTTTGG ATATTTTTT TTTTGAGCGG AGTTAGACAG	300
TGAGAGAGAG AGACAGAGAG AGACAGAGAG AAAGGTCTTC CTTTTGTTGG CTCACCCCCA	360
AATGGTTGCT ACGGGCTGGT GCGCTGCGCC GGATCTGAAG CCAGGAGCCA GGTGCTTCCT	420
CCTGGTCTCC AATGTGGGTG CAGGGCCCAA GCACCTGGC CATCCTCTAC TGCCTTCCTG	480
GGCCATATCA GAGAGCTGGA TTGGAAGAGG AGCAACCAGG ACAGAATCCG GCA	533

1123

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

GnGAGGCAnA GAGAGAGAGG TCTTCCATCT GCTGGTCAC TCCCCAATTG GCTCCAATGG	60
CTGGAACGTGA GCCAATCGGA AGCCAGGAGC CAGGAGCTTC TTCCGTGTCT CTGACACAGG	120
TACAGGGGCT CAAGAACTTG GTCCATCTTC TACTGCTTTG CCAGGCCATA GCAGAGTTGG	180
ATCAGAAATG AGGCAGCCAG GACTTGAACC AGCACCCACA TGGGATGCCA GCACTGCAGG	240
CAGCAGCTTT ACCCATTACA CCACAGTGCC AGCCCTTCAA CTATTTTAA TAGATCACTT	300
TTTTAAAAAT AGAATTATTC AGG	323

(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

ATGATAAAAAT ATTTGTAATG ATCCTTAAAAA TCTTCTTAGA ACAATTATGT ATGTATGTAT	60
GTAACAAATTC AGGTTTATTA TTTATAAGTT TGTTTCTTTG AAAGAGTAGG GGGCCAGCAT	120
TGGAGCACAG TAGGTTAACGC CACTGCATGT GGTGCTGGCA TCCCATATGA GCAGTTGTTT	180
GAATCCACTT CCAATCCAGC TCCCTGCTAA TGTGCCTAGG AAAGCAATGG AAGATGGTTC	240
AACTGCTTGG GTCCCTGCTA CCCTGTCTCT ATATGGAAA CCTAGATGGA GTTCTAGACT	300
CCTGGCTTCT GTTTGGCCCC ATCCTGGCTG TTGCAGCTAT TTGGGGAGTG AACCAAGCAGA	360
AAAGTTGTAAGT GTGATAGAAT TAGGACTTTA GTTATGGGAG GATAAAGCAA ATACATTTG	420
GTCTACAAGA ATCGCAGATT TGGAGAAAGT AAGAGTAATA AGGAAAAGTT TAAAAACTGT	480
AGGTGAGGCC GGCACCGCGG CTCACTAGGC TAATCCTCCA CCTAGCGGCG CGGGCACACC	540
GGGTTCTAGT CCTGGTCGGG GCGCCAGATT CTGTCCCGGT TGCCCCCTCTT CCAGGCCAGC	600
TCTCTGCTGT GGCCAGGGGA GTGCAGTGGGA	630

1124

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

CCAAGTATAA GCTCATGAAA GCATTTGTTT ATTTTATCTT TATTGATTTG CCTTTCATAC	60
TTAGACCTAT AATGTATCTG GGCTTGATTT TTGCATATAG TGTGAAATAG AATTCTACAT	120
ATCTGGGGCT GTTGCTGTGG CGTAGTGGGT AAAGCCACCG CCTGCAGTGC TAGTATCCCA	180
TATGGGCGCG GGTTCAAGTC CTGGCTGCTC CTCTTATGAT CCAGCTCTCT GCTATGGCCT	240
GGGAAGGCAG TAGAAGATGG CCCAAGTCTT TGGGCCCCCTG CACCCACATG GGAGACCTGG	300
AAGAAGCTCC TGGCTTTGGA TTGGCTCAGC TCTGGCCGTT GCAGTTAATT GGGGAGTGAA	360
CCAGCAGATG GAAGACCTCT CTCTCTCTCT GTGTAACCTT GACTTCAAA TAAATAATC	420
TAAAAAGTAC ATATCCAGTT GGATGAAACA CTTTATTGAA AAGACAATTG TCTGTCCCAC	480
TGCTATGTAG TATCTTATAA TTAGAACAAAT GACCATTAA TGACTGATCT GTTTCAAAT	540
TCTGnATTAA TCTGCTCCTG TCCTTTTAA nTTTT	575

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

AGGAAGACCT TTCTCTCTGT CTCTCTCACT GTCCACTCTG CCTGTCAAA AAAAAAAAAAA	60
AGGTATTTCT TCTGThGGTT CACCCCCCAA ATGGCTGCTA TGGCCGGCGC ACTTGCCGAT	120
CTGAAGCCAG GAGCCAGGTA CTTCTCCTGG TCTCCnATGC AGGTGCAGGG CCCAAGGACT	180
TGGGCCATCC TCCACTGCAC TCCTGGGCCA CAGCAGAGAG CTGGCCTGGA AGAGGGGCAA	240
CCGGGACAGA ATCCAGCACC CGGACCAGGA CTAGAACCAAG GGATGCTGGC ACCGCAGnGA	300
GnGATTAGCC TAGTGAGCCG CGGCCTGGC CACAACCCCT GAATTCTTGA CCTGTGGAAA	360
CAATCTAGTC AATTGTATT GCTGTTCAA GTCACTGCCT TATGGTCAT TTGTTTGCT	420

1125	
GCAGTTGACA ATTTAGTGTA TGTGGTAGGG TGGAAGAGCA TAGAACATGC TAGCTCCAGA	480
TAAAATTCCC GAGTCTAAGG TCGATAGCAG GGATACAGAG AAAGGAATCA GATTCTCTTT	540
CACTAGCAGG TCCAGACAAG CATAACAGCAG GCAGGTCAA CAAACAGGTG CTAGAGAGGG	600
GATGCCTCCT CCCCACTTCT CTTGGGTTTC CAGAGAAACC GATGGATTAG CCCCTGCTTG	660
TCTAAAAGAG GGGGGAAAAT AGCTTGAGAA T	691

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:

GAGAGAGAGA GAGAGAGAAA GGTCTTCCTT CCGTTGGCTC ACCCCCCAAA TGGCCGCAAT	60
GGTCGGAGCT ATGCCAGTCC GAAGCCTGGA GCCAGGTGCT TCCTCCTGGT CTCCAAGCG	120
GGTGCAGGAG CCCAAGTACC TAGGCCATCC TCCACTGCC TCCTGGTCCA CAGCAGAGAG	180
CTGGACTGGA AGAGGAGCAA CTGGGACTAG AACCCAGCGC CCATATGGGA TGCTGGCGCC	240
GCAGGA _n AGG ATTAACCAAG TGAGCCATGG CCCCCAGTAT AATGTTTAA GTTGTATTTT	300
TCCTGAAACA AAGAGTTGAG TGATAATGGA TTATTTGGAA AGTGATCCAG AATCACTGTA	360
TGGGAAAGTA GGAAAGAGAG TGGGAAACGA AGGAAGTCCA AACAGGGTAC AGGATTAATT	420
AATTAAGCTA TTACTGTGGG TAACGAAGGC TCAAGCCTAC TCAGGGAGAC TACATGAAAT	480
TTGCCCAACA GGTGCCTTAC CCAAGGAAGT TGGGGTATT ACAAATTCTGT ATCCCATCACT	540
GGATGATGGG CTTGCTTGAC TGAGTGGTTG TTAATTCCCT ACATAAGTGT GGACCTGCCT	600
CTCTCCTCCC CCTGAGAAAG CCTGAGGGGC AGAGCCACAC TGCTTACAGT AAAGAGATCA	660
CATGTTT	667

(2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

1126

nAACCTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC	60
TTTCTTTCTT TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTTTCTCTT TCTCTTTCTC	120
nnTTTCTCTC TTTCTCTCTT TCTTCAAGA TTTATTCAATT TATTATTTGA AAGGCAGAAT	180
TACAGACAGG CAAGGnAGAC AGAGAGAGGC TGTCCTCCA TGGGACGGTT CACTCCCCAA	240
ATGGGCAAAT CGACTGGAGC TGGACGGATC CGAACGCCAGG AGCCAGGAGC TTCTTCCTAG	300
TCTCCCATGT GGGTGCAGGG GCCCAAnGAC TTGGGCCATC TTCTACTGCT nTCCCAGG	358

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

TGATTGAAA CAAAATGTCT AAATCCTTCT AGAAAGTG TG TATTAATAA ATACGTAAAT	60
ACAAAACCCCT GACAGCTTCA TTCCCAAGAAA ACATCTCCTA TGCTGGTGA ACACAGACCC	120
CGGGGCCTCA GGCCAGnGA CCTGTCCAGC TCCTTGTTGT TTCTGATCAT GAAACAGGGT	180
TAAGATGTTG CACAGTCAGA CTCACCAGTC TCACCTCCTG GCCTTGGGA ATTATGCACT	240
GGAAGGCTGT CACATCTTCA TTTTTAAAG GAATTCAATT TTTTCAACCT AAATATCTTT	300
TATAAGAAAT AAGGCTGAGG CCGGCGnCGC GGCTCACTAG GCTAACCTC CGCCTAnTGG	360
CGCCGGCACA CTGGGTTCTA GTCCCGGTCA GGGGCCGGGA TTCTGTCCCA TTGCCCCCTCT	420
TCCAGGCCAG CTCTCTGCTG TGTCCAGGAG TGCAAGTGCAG GATGGCCCAA G	471

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

ATTTTTCTT TTTTAAAAAA CCTTTTTGG GGCCAGCACT GTAGCGTATG GnGTAAAGCT	60
GCCGCCTACA GTGTCAGCAT ACCACATGGG CGCCAGTTG AGTCCCGGCT GCTCTACTTC	120
CAATATAGCT CCCTGCTATG ACCTGGGGAA GCAGTGGAAAG ATGGCCCAAAG TGCTTGGGCC	180

1127

CCTGTACCCA CATGGGAGAC CCGGAAGAAG CTCCCTGGCTC CTGGCTTGG ATCAGTGCAA	240
CTCCAGCCGT TGCAGGCCATC TGGGGAGTGA ACCAGTGAAT GGAGGACCTC TCTCTCTCTC	300
TCTCTCTTTTC TCTCTGCCTC TCCTCTCTCT CTCAAATCTCT GCCTCTCTGT AACTCTGCCT	360
TTCAAATAAA TACATAATT TTTTTAAAA AACACCTCTT TCCTATTTTA TGGCATAACA	420
AGATGGTACC TTATACCTGT ACCTGCCCTG CCTGGGCCTG GGAATCACTC ACTTCTCTGA	480
GGGGCCTGTA TTCTGGTTTA ACAGACCAAG ATGTAAGTGC CAGATGATGT TTTTTCTGAT	540
GAGTAAAATC AATGGTAAAG CCATGTCTGT AAAGGTTGG TCTTTGATT ATTTTGCTA	600
AAGTATTACC TTTTTTTTT TGACAGGCAG AGTGGACAGT GAGAGAGAGA C	651

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

TCACATTGGG GGCCCAGTCA GTGGCTTAGT GGGTTAACCA GCCGCTTGCA GTGCCAGCAT	60
CCCATATAGA CACAGGTTCA AGTCCTGGCT GCTCCACTTC TGATCCAGCT CTCTGCTATG	120
GCCTGGAAA GCAGTAGAAC ATGGCCAAAT GCTTGGGCTC CTGCACCCAT GTGGGAGACC	180
TGGAAGAAC GCCTGGCTCC TGGCTCCTGG CTTCGGATCA GCACAGCTCT GGTGTTCTG	240
GTCATTTGGG GACATCTATC ATTAATTCAAG TAAACACATA ATCCAATGGA ATTTTAAGCT	300
CATGATATGT GTCCTACTAC CCATCCATT TTATTTCAA GACCTTTT TCTCTCTCTG	360
CCTCTCTTC TCTCTGTGTA ACTCTTTCTT TTTTTTTAAG ATTTATnTnC TTTATTTGAA	420
AGAGTTACAG AGCAAAGTAG AGCCAAAGGA GGAGAGAGAG AGAAAGAGAG AGAGAGAGAG	480
AGAGAGAGAG AGAGAGAGGT GTTTTCCATC TGCTGGTTTA CTCCCCTAAT GAnCAGAATG	540
GCCAGAGCTG TGCTGATCCA AAACCAGGAG CCAGGAGCTT CT	582

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

AAGATCTTTC TCTTTCCCCA TCTCCCTCTG TAACTCTGCC TTTCAAACAA AATAAATAAT	60
TTGTAAAAAG GCTAGTTAT TTGAAAGGCA GAGTTACAGT GAGAGACAGG GAGAGAGAGA	120
GCTTTCTCGT CCGCTGGTTC ACTCCCCAAA TGGCCACAAT GGCCGGAAGT GAGCCAGTCT	180
GAAGCCAGGA GCCAGGAGCT TCTTCTGGGT CTCCCATGTG GGTGCAGGGG TGCAAGCACT	240
CGGGCCGTCT TCCACTGCTT TCCCAAGCAC ATTAGCCGGG AGCTGGACGG GAAGTGGAGC	300
AGCCGGGATT CGAACCAAGTG CCCATATG	328

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

AGGAGAGGAC AACTTCTCTC CCGGGTAGGG GCTGAGTCTG ATTCCCTTTG GGGTCCGTCC	60
CAGAGCAGTG TGGTTTGGTG CTGAGTAGGG GAGGGAAGAA TGGAGCCTGT GAAAGCCCCT	120
GTGAGAGGGA CAGGAGAGCC CGGCCCTGAG CCCCAGAGCC CAAGCGCGGA nGnGCCAGG	180
CTCTGGAGTC CTGGGTGCTG GGTCTGGGTG TGCTATGATC TACAGAACCC CTGAGGATCC	240
TGACATGAGG GTCCATCTCT AGGCCCCAGA AAGTGGTCA TGGGAATGGT GAGCTTAACG	300
ACTCGGGGCC CAGCAAGGCC ATGAGAGAGG GGGATGGGG TAGGGTCCAG CTCCACTGTT	360
CCTTTTTTTG TTTGTTTGTGTT TGTTTGACA GGACAGAGAG AGACAGAGAG AAAGGTCTCC	420
TTACCATGGT TCACCCCCCA ATGGCCGCTG CGGCCAGCGC ACCGCGCTGA TrCCGAAGCC	480
AGGAGCCAGG AGCTTCTCCT GGTCTCCCAT GTGGGTGCAA GACCCAAGGA CTTGGGCCAT	540
C	541

(2) INFORMATION FOR SEQ ID NO: 718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

1129

GAGGTAAGTC TCATAATCCT ACAC TTTTG AAGTGAGATA ATACCTACTC CAGACAGTTA	60
ATGTGGATAT TAAATATGAT GTAACAAAC AGTGCCAGC ACATAGTAGA TGTTTAAAAT	120
ATGGAAGTTT TGGGGCTGGC ACTGTAGCTT ACCAGGCAA GCTGCTGCCT TCAGTGCTGG	180
CATCCCATAT GGGAACTGGT TCGAGACCCA GCTGCTCCAC TTCTGATCCA GTTCTCTGCT	240
ATGGCCTGGG AAGCCAGGGT AAGAGGGCCC AAGTCCTGG GCCTCTGCAC CCACATAGGA	300
GTCCTGGAAG AAGCTCCTGT CTCCCTGGCTT CAGATCAGCA CAGCTCTGGC AATTGTGGCC	360
AAATGGGAGA ATGAACCAGC AGGTGGAAGA CCTTTCTCTC CCTCTGTCTC TCCTCTCTCT	420
GTGTAATTCT GACCTCCAAA TAAATAAATA AATCTTTAAA AAATGCAAAG TTTCTCTCCT	480
CTCCACTACA CTCCAACCTCT TTCCCTCACT TAATAAATAA GACTCAGCTT GACCCCCACAG	540
GnACTCATCT TACATAGAAG AGCTAATACA TATGTCTAAA GCTGAAAAGT GAAGAAATGT	600
ATAGCAGACC TCTGCTCTCT	620

(2) INFORMATION FOR SEQ ID NO: 719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

GGCCCCAAGC ACTTGGGCCA TCCTCCACTG CACTCCGGG CCACAGCAGA GAGCTGGACA	60
GGAAGAGGGG CAACCAGGAC AGAACCTGGC GCCCTGACCG GGACTAGAAC CCGGTGAGCC	120
AGCGCCGCAA GGAGAGGATT AGCCTGTTAA GCTGTGGCGC CAACCTGTAT ACAAAATTAA	180
AGTATGATTT TGTTTGGTTG GTTTTTGAG GTATAATTAA AAAAAAAA GCTGTCTTT	240
CCTTTCTTG CTTTGTTTC CGAAAAGCTA TCACGAGAGA AAACAAACCTT TGTTTTTAA	300
AGTTTAAAAA ACTTGCTTTG ACAAAAGCTA ATAAATTATT TTTATTAA AATCAAATTAA	360
ATATACTTTG GGGCGGTGCT GTGTACAGCA GGTGAAGCCA CnGCTGTGGT GCGGCGTCCC	420
ATATGGCAC CAGACGCCA TCAGCCCCAA CGCCACAAGC ACTACCGnAC CCAACAGGCA	480
CCTGCCACCC CACGCAGACG CATCAAATGG GCTCCTCCTG CCTCGCCGTT AG	532

(2) INFORMATION FOR SEQ ID NO: 720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1130

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

AACGGGnCTG	TGTGTTAGGAT	GTTAAGCTTC	TGCCCTGTGGT	GACGGCATCT	CATATGGATG	60
CCGATTCAAG	ATCCAGATGC	TCCACCCAAT	CTAGCTCCCT	GCTAATGGCC	TGGGAGAGCA	120
GTGGAAGATG	GCCAGAGTAT	TTGGGCCCCCT	GCACCCACAT	GGTAGAGCCA	CAAGAAGCTC	180
CTGGCTCCTG	GTTTTGGATG	ATCCCAGCTC	TGGTCATTGC	AGCCATTGG	GGAGTGAAACC	240
AGTGGACGGG	AGATCTCTCT	TTCTGTCTTT	CCCTCTGTCT	GTAACTCTGC	CTTTCAAATA	300
AATAAATAAT	TTTTAAAAAT	AAATCTTCT	TTAAAAAAAAA	GGGAAAACAT	GGGGCTGGTT	360
CTCTGATGTA	GTGGGCAAAG	CTGCCACCTG	TGGTGCCAGC	ATCCCATATG	GGCGCCAGTT	420
CCTGTTCTGG	CTGCTCCACT	TCCGATCTAG	CTCTCTGTG	TGCCCTGGGA	AAACAGTGGA	480
AAATGGCCCA	ATCCTTTGGG	CCCCTGCACC	CACGTGGGAG	ACCCGGAGGA	ACCTCCTGGC	540
TCCTGGCCTC	AGATCAGCCC	AGCTCCGGCC	GTTGTGGCCA	CTTGGGGAGT	GAGACAAAAG	600
AT						602

(2) INFORMATION FOR SEQ ID NO: 721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

AGTACAAGGG	GGGCTTCAAC	GAGTCATGG	AAAAATAGAC	TCAAAATGC	TTAATTTTTG	60
AAATCCACGC	ATAGTTACTT	CTTGAAGACC	CTGTCATGTA	CTAGCACTCT	GCCTCCTCTG	120
GCCTATTACG	TTAAAAACAA	CAACAACAAC	AAACAACAACA	ACAACAACAG	TTCACCTTT	180
GCCTAGTAGC	TCAGGTATCA	CTTCCTCTGG	GAAGACCACC	AAGAATACAA	TCAGAGAAC	240
ATGAAACACA	TAAGGAAACG	GTAACCTGTG	ATACACTCAC	ACCAAGAAGT	ACAACACAAC	300
CATTAATAT	CATATTTATT	TTATTGGCAT	AGGAAGAAAG	TTGGCATTAA	AAATATGTAT	360
ACGGGGGCCA	GCACGTGGT	GTACTGGTA	AGCCACTACC	TGCAGTGCCA	GCATCCATTA	420
TGGGTGCCAG	TTCAGGTCC	GGCTGCTCCA	CTTCCAATCC	AGCTCTTGC	TATGTCTGG	480
GAAAGCAGCA	GAAGATGGCC	CAAGTCCTCG	AGCCCCTGCA	CCCACGTGGG	AGACCCGGAA	540

1131

GAAGCTCCTA GCTTTGGATT GGTGCAGCTC TGGCCATTCG AGCCATCTGG GGAGTAAACT	600
AGCAGATGGA GGACCTCTCT GCnTC	635

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

ATCCTCTGCC TCTGTGAAC TTAATATGTG TGGTTCCCTCT TCTACGCACC AGACTGCATG	60
CTAGCTGCCA TCCACACAAT GTGCTCCCCC TGCCAACAGC CATAGGTCAT GTTCCAATGT	120
CAGCATTACT ACTGTTCACT TTAATATATC TAAAATCTAA CATAAAAGTA TTTATAATGG	180
GCTGGCCCTG TGGCACAGCA GGTTAACGCA CAAGCCTGAA GCCCCAGTAT CCCATATGGG	240
CACCAAGTTCT AGTCCTGGCT GCTCCTCTTC TGATCCAGCT ATCTGCTATG GCCTGGGAAG	300
GCAATAGAAG ATGGCCAAG TACTTGGCC CCTGCACCCA CATGGGAGAC CGGAAAGAGG	360
CTCCTGACTT CGGATCAGTG CAGTCCAGC CATTGTGGCC ATCTAGGGAG TGAACCAGCA	420
GATGGAAGAC CTCTCTCTCT GTCTACCTCT CTCTGCAACT CTGTCTTCA AAAAAATCTT	480
TTAAAAAAAAA GTATTTGTAA CAATAATGGT GCTGTACCCA TGGCACCTAC TGTCTCCTTT	540
CAAGTCTGTA CTCTGTAAA TGGAAAGTAAC ACAGTTCAAGA ACAGGTTTAT GGGCTACAGT	600
GTGACACCTT CATGCATGTA TATGATGTGT GCT	633

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

TTCCCATTTC CATTGGTCT TAAGCACTAG ATATAACTAT TGTTATCATT TTCCAGATGA	60
AGAGGAACAG AGATTACCCA AGATGCTATT GCTAAGCATG ACAAAAGTCAG CATTCAAACC	120
TGGAAGCATT TCTTAATGAC GATGGTTAAT TTTTGTGTTGG ATTTGTCAGT CTAGTTGATT	180
GTATATACTA TATATATATA TATATATACT GTCTACAGAT TCCAAAAGGT TTTCCCTTTAA	240

1132

AAAGATTTAT TTATTTGGCC GGCACGTGCG CTCACTAGGA TAATCCTCCA CCTTGGGGTG	300
ATGGCACACC GGGTTCTAGT CCTGGTCGGG GCGCCGGATT CTGTCCCGT TGCCCCCTCTC	360
CCAGGCCTGC TCTCTGTTGT GTCCAGGGAG TGTAGTGGTG GATGGCCCAA GTGCTTGGGC	420
CCTGCACCCC ATGGGAGACC AGGATAAGTA CCTTGChCCT ACCATCG	467

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

CGTACCCAT TGTATTATTT CAAATACAT TCAAAATATGT ATCCGCTCAT GAGACAATAA	60
CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATCAGCCT	120
TCTTTCAAGC TTCCTCCTTG GCGCCCGAGG CACAGnGAGC CGAGCATAGC CGCGCAGGCA	180
AGTGC	185

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

CGGTACCTGG TCAGTTTGCA AACGCCACG GTGGAGATGA GCGGCTTATA TTCCTCAGGA	60
GCGTGTGGCA GATTGTGGTG AAAGCGAATG GGTGTTGATA ACCGGGTTCA GGGTAGAATT	120
CCCAGCCGCC TGGTGGCGAA GCCGCCCGGC GCCCCAAATT TTTCCCGGCG GTTGnGCCCT	180
TACnGGTTC	189

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

TAATTATGAA AACTGAATCA AGAAGACATA GAAAATCTGA ATACACTTAA AAAAAGAGGT	60
TGGATTAGTA ATTAAAAATT TCACACAAAG AAAAGTCTAG TCCCAGTTAT ATACTTTTTT	120
TAAAGATTAA TCTATTTATT CAAAAGTCAG AGTTACACGG AGAGAGGAGA GGAGAGAGA	180
GGCTTCCAT CCACTGGTTC ACTCCCCAGA TGGCCGCAAC GGCCAGAGCT GTACCGATCT	240
GAAGCCAGGA GCCAGGAGCC TTCTCTGGGT CTCCCATGTG GGTGCAGGGA CCCAAGGACT	300
TGGGCCATCT TGTACTGGTT TCCCAGACCA TAGCAGAGAG CTGGATTGGA AGAAGAGCAG	360
nTGGGACTCG AACCAAGCCCC CATATGGGGT GCCGGCACTG CAGGCCGGCGC TTTAnCCGCT	420
ACGCCACAGA GG	432

(2) INFORMATION FOR SEQ ID NO: 727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

TCCTCCTGCA GCGCCAGTAT TCCATATGGA CACCAGTTCT TGTCTGGCAG TTCCACTGCC	60
AATCCAGCTC TCTGCTATGG CCTGGGAAAG CAGTGGAAAGA TCATCCAAGT CCTTGGGCC	120
CTGAACCCAC GTGGGAGACC TACAAGAACG TCCTGGCTTT GGATCAGCAC AGCTCCAGTC	180
GTTGCAGTCA TTTGGGGATT GAACCAGTGG ATGGAAGACC TCTCTGTCTT TACCTCTCTC	240
TGTCTGCAAC TCTGCCTCTC AAATGAATAA AATCTTTAA AAATTTTTAT TTATGTCTGT	300
ATTTTATTTG AAAGAGATGA GGAGGGAGAG AGCGTGAGAG CCAGTGCACA TGATACCTTT	360
CAAUTGGTAG TTCACTGCC CGTTGGCCTC AATGGCCAGG GCTAGGCCAG GCCAAAACCA	420
AGAGCTTC	428

(2) INFORMATION FOR SEQ ID NO: 728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

1134

TTTACTTGCT ATGTTCACAG TTCCCTACAGG AAAACTTGGA ACACAATAGA CATTCAAGCT	60
TTATTTGTTG AAGATTATGA ATATTTAGGA TGAGACACTG TGCTTTACGT TCCCCCCCCTA	120
AATCCCAAAG AAATGATATT ATTTGTGTA TAAGTGACTT AAAACATATT TTCCCTGAGGC	180
CAGTATTGTG GCATAGCAAC TAAAACGTGCC ACCTGTGATC CCGACATCCC ATAGGGGTGC	240
CAGTTTGAGA CCCGGATGCT CCACCTCTGA TCCAGCTCCT TCCCTAATGC ACCTGGGAAA	300
GCAGTAGAGG ATGGCCCAAG TGCTTGGGCC CCTGTACCTA CGTGGAAAGAC CCATAAGCTC	360
CTGGCTCCTG GCTTTGGCCT GGCCAGCTC CAGCTGTTAC AGCCATCTGG GGAGTGAACC	420
AAAGGATGGA AGACCTCTCC ATGTCTCTCC CTCTCTCTGT GTA	463

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

AACTCACGCA AAGAGAAATC GACAATATCA ACAGGTGTGT GTTTAAAAAA ATTGAATCCA	60
TAATTAAAC CTTCCAAAAC AGAAAGCACA AGGCTCTGAT GACTTCATTC AACATTCAA	120
TGAGGTATAG GAGCAGGTCT TTGGCCTAAT GGTTAAGATG TCCACGTCCC ATATTGGACT	180
GACTGGGTGT GATCCCTGGC TCTAGACTCA ATTTCAGCTT TCTGCTGATT TAGACCCCTGG	240
GAGGCAGCAG GTCATCATTC AAATGGTTGG GTCACCTCCA CCCATGTGGG AGACATAGAT	300
AGAATTCCCTG GCTCTTGTCTT CTGGCCCTGG CCCAGCCTAC CAGTCATTTC AAGCATATGA	360
AATGTGAATG AAAAATTAGA ATGTGTGATC TCAAATAAT AAATACTTAA AAAAAAAAAAA	420
AAACTAAATT ATCTAGGGCT GGCAGCTGTGG CACAGTGGGT TAACGCCCTG GCCTGCAGCG	480
CCAGCATCCC ATATGGAAGC CGGTTCTAGT CCCAGCTGCT CCACCTCCAA TCCAGTTCCC	540
TGCTATGGCC TGGGATAGCA ATAGAAGATG GCCCAAGTCC TTG	583

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

TTGGAGTTGT AATAAAAGGA ATTTTCCCTT CTACCTCCTT TCTGTAAGAA ACATCAGGCT	60
TTCTGCCAC TGGTTAACACA TGATTAAGTG GTAAACAGTG ATGAATATTT CCCAGATAAC	120
TACATCTCAT GATGTTTTT TAAAGATTAA TTTATTTATT TGAAAAGTAG AGTTAGAGAG	180
AGAGAGAGAG AGGCCTTCGG TCTGCTGGTT CACTCCCCAA ATGGCTGCAA TGGATGGAGC	240
TGGGCTGATC CAAAGCCAGG AGTCAGGAGC TTCTTCTGGG TCTTCCACAT GGGTGCTGGG	300
GCCCAAGGAC TTGTGCCATG TTCTACTGCT TTTCAAGGCC ATGGTAGAGA GCTGGATCAG	360
AAGTGGAAACA GCAGAGACTT GAATTGGTGT CCCTATGGGA TnCTGGCACT GnAGGCGATG	420
GCTTTACACA CAATGCCACA GTGCCAGTCC CTCATGATAT TTTTATTAAT GTTAATAGGn	480
TTCTGGTGGG CAAAAAAATAG TTTTGTAGAA AAATATTTTG GGAATACACT CAGATAACAT	540
TTGAGCAAGT TTCTTCCCTG CAGGACATAT CAGACAnTCA ACTATATTAn	590

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

ATGCAAAAT ATATACTAAA GGAAAGTTTT CAGGCAGAAG GAACATTGTA TCAGAAACTT	60
GAAGCTAAAC AAAGGCAGAG CACTAGAAAT GGAAAATAGT AAAATAAAAT TCATTTTTTC	120
ACAGTTTGAG TTGTTCTAAA AGATAACTGA CTTCAGGGC CGGTGCTGTG GCACAGCAGG	180
TGGAGCTGCT GCCTTCAACA TGCCATCATC CCCTATGGGT GCCTGTTCAA ACCCTGGCTG	240
CCCCATTTCC TATTCAGCTC CTTGCTGGTG TGCCTGGGAG GGCAGCGGAA GATGGCCCAA	300
GTGCTTAGGC CCCTGCACCC ATGTGGGAGA CCCAGAGGAA GTTCCTGGCT CCTGGCTTG	360
GACTGGTCCA TCCCTGGCTG TTGTGGCCAT TTGGGAATG AATCAGCAGA TGGAAGATCT	420
CTCTTTCTCT GTCTGCTGT CTGTCCTCT CTGTAATGCT ACCTTTCAAA TAAAAAAAGTC	480
TATTTTAAAA AGATAACTGA TTTTCTAAA TGGTAGAAAT GCATTATGTG TTTATAACAT	540
GTAAAAATAA AATGTATAAC AAATATAGCA CAATGGATTG GATAGAGGAA TTATGAAAAT	600
TCCTTTAACCA TAGAATCATT ATATGTTACA TGAAATGTG TAATATTATT TGAAGGnAGA	660
TTCTGATTAT ATATGCGTAA GGATAAACCC TAAGACAACT GCTAAAACAA	710

1136

(2) INFORMATION FOR SEQ ID NO: 732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

TTTCACAGCA AATGCAACAA TTAGAAAGAGA CACCTACAGA ATAGGAGAAA TTATTTACAA	60
ATCATACATA TAACATAGTG AGAATATCTG GAATATATGA AGAACTTAAT AGTAACCTAA	120
CCCCCCAAAT AATTTGATTT AGAAATGGGC AAAGGTGGGG CCGGGCCTGT GGCTCAGTGG	180
GTAAACACCC TGGCCTGAAG TGCCAGCATC CCATATGGGC GTCCGTTCGA GACCCGGCTG	240
CTCCACTTCC AATCCAGCTC TTTGCTGTGG CTTGGGATAG CAGTAGAAGA TAGCCCAAGT	300
CCTTCGGCCC CTGCACCCGC ATGGGAGACC CAGAAGAAC TCCTGGCTCC TGGCTTCGGA	360
TCAGAGCAGC TCCAGCCGTC ACGGCTAATT GGGGAGTGAA CCAGCAGATG GAAGATCTCG	420
ATCTCTCTCT CGATCTCTCT CTCTCTCTCT AACGCTGACT TTCAAATAAA TAAATAAAATC	480
TTTTTTTTAA AAAATGGGG CAAAGGGCAT GAATAGACAC AGATATCCAA GAAGTATCTT	540
AAAAATGCTC AACATTACTA ATCATCAGAG AAATGCAAGT CAAAACCTCA TTGAGATATC	600
ACTTCACCCA GTTTTTTTTT T	621

(2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

TCAGAAATCA TATTTGAATT AAAATCTTTA AAATGGAGAA GCAACATCAT CTGAAGTATA	60
ATAATAACTA AGCATTAA ATTGTCAGAT ACAGGAAGCC ATAGAGGAGA ACAAGAGAAA	120
AAAAAAAAAG GACTGAGGCC AATGATGTGA TGTAGTGGGC TAAGGCTCCA CCTGCAGTGC	180
CAGCATCCCA TATGGGTGCC GGTTTATGTC CCAGCTGCTC CTCTTCCAAT CCAGCTCTCT	240
GCTTATGGCC TGGGAAAGTG GCAGGAGATG GCCCAAGTGC TTGGGCCCCGTACTTGTGT	300
GGGAGACCCA TATGGATTTC CAGGCTCTTG GCTTTGGCCT GACCCAGCCC CAGCCATTGC	360

1137

AGCCATTGGA GGAGTGAACC AGTGGACGGA AGACCTCTCT CTGTCTGTCC CTCTGCCTGT	420
AGCTCTAACCA TCTCAAATAA ATAAATAAT CTTTAAAAAA GGAnGGGGGA GGAAGAGAAC	480
AAGAAGAAGA AAAAGAACCTT ATGAAGAGGA AAGGGATGAA CCTATAGAGT ACTGGTAAAC	540
ACTGGGTTCA CATTTCAAAC CCAAGGCTGC CCATGGCAGT nAGCATTCAC TCTAAAAGGG	600
AGCATG	606

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

TGCTATGCC TGGGAAAGCA GTAGAAGATG GCCCAAGTGT GTGGGCCCCT GCACCTGTGT	60
GGGAGACCCA GAATAAGCTC TTGACTCCTG GCCAAGATTG GCGCAGTTCT GCCCACAGTG	120
GCCATCTGAG AAGTGAACCA GCGGATGGAA GACCTCTCTC TCTCTCTCTG CCTCTCCTCT	180
CTCCGTGTAA CTGTGACTTT CAAGTAAAAT AAATACATAA AAAAAAAA AAAAGAAAGA	240
AAGAAAGAAA GAAAGTAAAC AGCTAGGTTG CTAGACACCA GAATCAGGAT GCACCATAGG	300
TTCCTTACAT TGGAGAGTGG CATGGGAAG TGATTGCTGG AGAAATGGTG AAGGnGACTA	360
TGAAAACCTTA ATCTAGAATA ACCTGTACCT TTTCCGAATT TACCATTCT TGTTGAGATT	420
TAGGAGGnTA ATAACCAACA CCCCTTCCTC GnTCCCCCAA ATGTGG	466

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

ATGCTACATG ATAATTTCAA GGGAGAAGCC AGTAGAGAAC AAACAAGAAC CCTAGAGATT	60
CTCCAAATGC ACAAAAATGC TGCCGTTCCCT GAATTGCAAG CTGACTTGAA GCAGAGGAAT	120
GAGATTTCCCT TTCCAAGTTA AAACAAATGC ACAGATTATC ATTGACTTCT TTCATTAAAA	180
GCATTTATTT TATTTATTTG AAAGAGTTAC ATAGAGAGGT AAAGTCAGAG AGAGAGAGAA	240

1138

AGAGGTCTTC CAACAGCTGG TTCACTCCCC AAATGACTGC AATGGCCAGT GCTGAGCTGA	300
TCCAAAGCCA GGAGCCAGAA TCTTCTTCTG GGTCTCCCAT GTGGATGCTG GGGCCCAAGG	360
ATTCCGGCCA TCTTCTGCTG CTTTCCCAGG ACATAGCAGA GAGCTGTATC GGAAGTGGAG	420
CAGCTGGGAC ACGAACTAGC ACCCACATGG GATGCCAGAA CTGCAGACCA AATCTTTAAT	480
CCATTGTGTC ACAGCACCCAG CCCTTACCAATT AAGTTCTTTT TTTTTTTTTT TTGACAGGCA	540
GAGTGGAnAG TAAGAGTGAG AGTGAGA	567

(2) INFORMATION FOR SEQ ID NO: 736:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

GAATTCTTC TGGCTTCTAG GGTGTTGTCC CAGGTCTTCC TCCTGAGGTT ACCTTCAGAT	60
GTTAGAACATAG AAGTTGCAGG GCCAACGCTG AGGTGTGGCG GGTAAAAGCT GCCGCCTACA	120
GTGCCAGCAT CCCATATGGG CACTGGTTCG AGTCCCGGCT GCTCCACTTC CGATCCAGCT	180
CTCTGCTGTG GCCTGCGAAA GCATAGAAGA TGGCCCAAGT TCTTGGGTCT CTGCACCCAT	240
GTGGGAGACT CTGAAGTAGC TCCTAGCTCC TGGCTTCGGA GATCAGCACA GCTTTGGCGG	300
TTGCGGCTAA TTGGGAAGTG AACCATGGAA TGAAAGACCT CTCTCTCTTC nCTCTCTCTC	360
TGGCTTCTCC TTCTTTCTCT GTGTAACCTCT TTCAAGTAAT AGTTAAATAA ACCTTAAAAAA	420
AAAAAAAGAAT AGAAATTGCA TCTTTTCTA GTTAGAGCAA GCCTGAGTCT CATTCCCTCAC	480
AACTTTAAAG ATGGCTCTTC TCACCTGCAT AATGCATCAA GGTCTCCTCT TTTACTA	537

(2) INFORMATION FOR SEQ ID NO: 737:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

TAACAAAGTG AAGAGGTAAT GAAAACAATG AGAGAAAAATA TTTGAAAACAT ATGCATCCAA	60
TAAAGGATTA ATATCAAGAA TATATAAGGA GTTCCAGAAA CTCATAACA ACAAAATAAT	120

1139

CCAGTTAAAA ATGTGCAAGG GCAGGAACAA GCATTTTCA AAGGATGAAA TAAAAAGGGC	180
CAACATGGGG CCAGCACTGT GGACATAGCA GGTAAAGCCA CCGCCTGCAA TACCACTATT	240
CCATATGGGT GCTGGTTCAA GTCCCAGCTG CTCCACTTCT GATCTGGCTC TCTGCTATGG	300
CCCAGGAAAG CAGTAGAAGA TGCCCCAAGT CCTTGGGCCCT CGCACCCAC CTGGGAGACC	360
CAGAAGCTCC TGGCTCCTGG CTCTGGACTG GCTCAGCTCT GGCCATTGnC AGCCATTGG	420
GGAGTGAACC ATTGGGTAGA AGCCCCCC TCTGTGTGTA ACTCTGACTT TGAAATAAAT	480
AAATAAATCT TAAAAAAAAA AAGGCCAACA GACAGATGAA AAAACTCCAG GATGACTGCC	540
ATCAGGGAAA TGCAAATACA AATTACAGTG TGGTGTCAACC TTACCCAGC TAGAATGCTA	600
TCATTCAAAA ATCAAAATG GA	622

(2) INFORMATION FOR SEQ ID NO: 738:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

GAGCAAAGTG GCATTGAGAA GAAAAAAATC GCCACATTTT GGACACTTTC CACAACCCCTA	60
ACTATTCTTT TGGATTATGA TTTTGTGGG TTTTGTGTTA AAGATTTTT TATCTGTTTA	120
TTTCACAGGT AGAGTTAGTT ACAGACAGTG AGAGAGGGAG ACGGAAAGGT CTTCCCTCCA	180
TTGGTTCACT CCCCAAATGG CCACCACAGC CAGAGCTACG CCGATCCGAA GCCAGGAGCC	240
AGGTGTTGTC TCCTGGTCTC CCATGTGGGC GCAGGGGCTC AAGCAGTTGG GCCATCCTCC	300
ACTGCCCTCC CAGACCACAG CAGAAGGTGC TGGACTGGAA GAGGAGCAAC TGGGACTAGA	360
ACCTGGCACC CAACCTAACAT ATTAATCCAT AAATACCTTA AATATATCCC CCTGGGAAAT	420
CTTGGAGAGT TTATATACTA GAAAAGCAT TTATTGATGA TTTAAAATTT TTTTAAAGTT	480
TATAAAAACA TAACATAAAAT CTTACCTTAA ATATCTGTAG nATGGGGTAn CTC	533

(2) INFORMATION FOR SEQ ID NO: 739:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

TTTGTGCCA CAAATGCCA TTCTCGGGC TGGCGCTGTG GCACAGTGGG TTAACGCCCT	60
GACCTGAGGC ATTAGCATCC CATGTGGCA CTGGTTCAAG ACCCAGCTCT CTCCTGTGGC	120
CTGAGAAGGC AGTAGAAGAA AGCTCTAGTC TTTGGGCCCC TGACCCATG TGGGAGACCC	180
AGAGGGAGGCT CCTGGTTCT GGCTTCGGAT CAGCACAGCT CCAGCCATCG CTGCTGGTTG	240
GGGAGTGAAC CATCAGATGG AGGACCATTG TCTCTCTCTC TCTCTGCCTC TCCTCTCTCT	300
GTGTAACTCT GACTTCAGA TGAATAAAATG AATCTTAAA AAAAATGCC CACTCTCTAC	360
ATAATGCTTT AAGATTCACT CATGATAGAG TACATGTGAT ATTTTGTTA TTACTGAATA	420
GTATTCCAAG CATGTGGTTT TGAAGGGACT AAATGAGCAG TTCTGCCAA GGCTGGCTCA	480
CCTGGATCTT CCTTAGAGAC GAAATCCTAC AGCCCTC	517

(2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

AGACCTTTCT CTCTGTCTCT CTTTCTCACT GTCCACTCTG CCTGTAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAGGAAAAA AAAGGAGAGG AAAGGATAAG GCCCCTGGGA GTGCTGTTCC	120
CTGGAATACA GTAAGGGGTG GCTGCTGGCT GCTCTCTGGG CTGTGGGCCT GGGTCAGCCC	180
AAGGTTCTTG GGGAGATACG CAGCTGGGT TGTCAGAGTT AGCTCAGGAG AGAACTTACT	240
CCTCAAGCAC ACTTAGAGTG AACCTTGCT AAGTTGGCTA CACAACCTCT CTATTCTGTA	300
AACCAGTTGA AATAAAATCTT ATGGGTTTTG TTTGAAAGGA ATTTATATGA GCAATTTTAC	360
TAAATCAGGA ATATTTTAA AGATTGTTA TTGGGGCCAG TGCTGTGGCA GCGGCTCCTC	420
TTCAGATCCA GCTCCTGCTA ATTTGTCTGG GAAAGCAGTA GGAGATGGCC CAGGTGCTTG	480
GCCCCTTTAC TCACATGGGA GACCTGGAAG ACGCTCCTGG ATCCTGGCTT CAGCTCGGCT	540
CAGCTCTGGG nGTTGCAGCC ATCTGGGGAG TGAACCAACA GATGGAAGAC CTCTCCTTCT	600
CTCTGCCTCT GCCTCTATAA nTCTGCCTTT CAAATAAATA AAT	643

(2) INFORMATION FOR SEQ ID NO: 741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs

1141

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

TGCCAGTTCG AGTCCCGACT GCTCCACTTC TGACCCAGCT CTCTGCTATG	60
GCAGTGGAAG ATGGCCCAAG TCCTTGGGC CCCTGCACTC CCATGGGAGA CCCAGAAAGAA	120
GCTCTTGCT CCTAGCTTG GATGGCTAG GAGCTCCAGC TGTTGCGACC AACTGGGAG	180
TGAACCAGCA GTTGAAGATC TCTCTCTCTC TCGGCCTCTC CTTCTCTCTC TCTCTGTGTA	240
ACTCTGACTT TAAAATAAAT AAGTAAATCT TCAAAACAAA AACAAAGTTT GGTTCCAATT	300
ATGATTACTT TGTTATTGCC AGTTTGTGA TTAGGGTTCA CTTAAAACGA GATACTGTAA	360
ATCTGAGAAT ATACAGGGGC ACCTGGCGTC ACATCACAAA AAGTCTGGCA CATTTCAGTT	420
TATTCAAGCA ACTATCCATG ATCTACATAG CTAAATGAAA CCTTATTCTG ATCTAAATAG	480
GCATCTGCCT CTAAATATTT TAATATGCAA TTCTGTCTCT ATTCTAATAA T	531

(2) INFORMATION FOR SEQ ID NO: 742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

AGGGAGTTTT TCCCTATGGT TGACCAAAAG ATAATAAAAC TACCTTGCTT ATTCAAGACAG	60
AACGCAAAAT CAGCATTCCCT CTCTTCAACT GCTCAGCTGT AGGTCAATTG ATCCAACACCG	120
TCCTATAAGT TAACATTTAA TATTCCAGT GGATCTATTA AATTTTATTT GCGGAAGTGA	180
TTTCTTTTA AGATATATAT GTATATATAA ATGCTTATTT TAAAAAATAT TTATTTGAAA	240
GGCAGGGTTA CATAGAGGCA GAATTAGAGA AGAGAGAGTG AGGTTTCTA CCCATTGGTT	300
CACTTCCCAA ATGGCCACAA TGGCCGGAAC TGCGCCGATC TGAAGCCAGG AGCCAGGAGC	360
TTCTTCCAGG TCTCCCACGT GATTGCAGGG ACCCAAGCAC TTGGATCATC TTCTGCTGCT	420
TTCTCAGGCC ACAGCAGAGA GCTGGATCAG AATTGGAGCA GCCAGGACTC AAAATGGTGC	480
CCATATAGGA TGCTGGCACT GCAGGCAATG GCTTCCCTCT GTATGTCACA GTGCTGGCCC	540
CAAATGCTT GTTTTATAT ATGTGTTTAT GTGTGTATTT TAATTGGAGA GGCACAGAGG	600

1142

633

GAGAGAAAGC ATGCTACTAC CTGCAGGnTC ATT

(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

TTATCATGTA ACACCACCCn TGCAGCCAAC TCAGGACCCC CCAACAAAGG TCACCACCAG	60
ATGCAACCCC TCGACCTGAG ACTTCTCTGT CTCCCAGAAT TATAAAAAAA TATACATTTC	120
AGGGCAGGTG TTTGGCGCAG TGGGTATAGC TCTGACCTGT GATGTTGGCA CCCATATGGG	180
TGATGCTCCC TGTCCCAGCT GCTCTGTTTC CAATCCAGCT CCCTGATAAC GACCCAGGAA	240
AAGTAGCAGA AGTTGGCCCA AGTGTGGGG TCTCTACCAC TTGTGCGGGG GACCTTAATG	300
AAGCCCCCTGG CTTAGATCTG GCCCAGCTCT GGCCATTGCA GCCATCTGGG GAGTGAACCA	360
GTTGGATGGAA GATGTCTCTG TTTCCATCTC TCCTTTTTTC TCTGCAACTC TTTCAAATAA	420
ATAAAATAACA CACATTACTT AGCTTTGTGA ATTGCTTGAT CTCAGGTATT TTGTTTTCTA	480
AGAGAGAACCA GGTAAAGATA TAGAGAGTGA AACCACCATA TGCAGTGCCG GTATCCTAAG	540
GGTGTGGTT CGAGTCCCCG CTGTTCCACT TCCAATCCAG CTCCCTGCTG ATGCACCTGG	600
GAAAGCAGGG GAAGGTGGGC CAAGTGTTG GGACCCCTGAA CCCATGTGGG AGACCCAGAA	660
GAAGCTCCTG GCTCCCAACT T	681

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

TGGCCATCAA CATGGGGAAC TTGGATTGAA TTCCTGTATT CTGATTTCAC TTTTACCCAG	60
TCGTAGTCAT TGTGGACAAT GCTGAATGAA CCATTGAGTG TGAATGTGTT ATAATAAAAC	120
TGTATTTGAA AAAGGATTGA TTTTTGTAGA CCAAAAATTA AATAAAAATA AACAGAAAAG	180
ATTAACACT TGATTTCTTC CTGAAAACAT GGTGAACACC TTAGAACTGG GATGCTCCAA	240

1143

TATGACTTGG AGTCTCAGAA TATAAATAAA GATACTTAGG AAGAAAAGTA GCCTTTATCA	300
CATTACTTTT TTTAAAAAAA TATTCATTTA TTTATTTGAA AATAAGAGTC AGACACACAC	360
ACACACACAC ACACACACAC ACACAAAGAT CTTTCATCTG TTGGTTCACT CCCCAAATGG	420
CCACAATAGC CAGAGCTGAG CCTATCTGAA GCCAGGAGCC AGGAACTTCA TCTGGGTCTC	480
CTACAnGGGT GCAGGAGCCC AAGGACTTGG GACATCTTCC ACTGCTATCC CAGGCCCGTC	540
TGCAGGGAGC TGGATCAGAA CTGGAACAGC TTGGGACATG AACTGGGCAC CCACATGGGn	600
TGCTGGGCAC TGCAGATGGT GACTAAACCT GCTGCATCAC AGTGCCTGCC C	651

What Is Claimed Is:

1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-744, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-744 depicted in Tables 2 and 3 or a degenerate variant thereof.
3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *T. pallidum* genome of commercial importance comprising the following elements:
 - a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS: 1-744;
 - b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *T. pallidum* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS 1-744: with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
7. A method for identifying an expression modulating fragment of *T. pallidum* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS 1-744: with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *T. pallidum* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS 1-744: depicted in Tables 2 and 3, or a degenerate variant thereof.

9. A vector comprising any one of the fragments of the *T. pallidum* genome SEQ ID NOS: 1-744 depicted in Tables 2 and 3 or a degenerate variant thereof.

10. An isolated fragment of the *T. pallidum* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a degenerate variant thereof.

11. A vector comprising any one of the fragments of the *T. pallidum* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *T. pallidum* genome of claim 8.

13. An organism which has been altered to contain any one of the fragments of the *T. pallidum* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *T. pallidum* genome depicted in SEQ ID NOS: 1-744 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *T. pallidum* genome of SEQ ID NOS 1-744: and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

- a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-744 and Tables 2 and 3, including fragments thereof;
- b) identifying members of said library which contain sequences that hybridize to said target sequence; and
- c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *T. pallidum* genome of SEQ ID NOS: 1-744 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

1146

- a) isolating mRNA, DNA, or cDNA produced from an organism;
- b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *T. pallidum* genome to prime said amplification;
- c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *T. pallidum* genome of SEQ ID NOS:1-744 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

20. A method for producing a polypeptide in a host cell comprising the steps of:

- a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *T. pallidum* genome of SEQ ID NOS: 1-744 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

- b) isolating said protein.

Figure 1

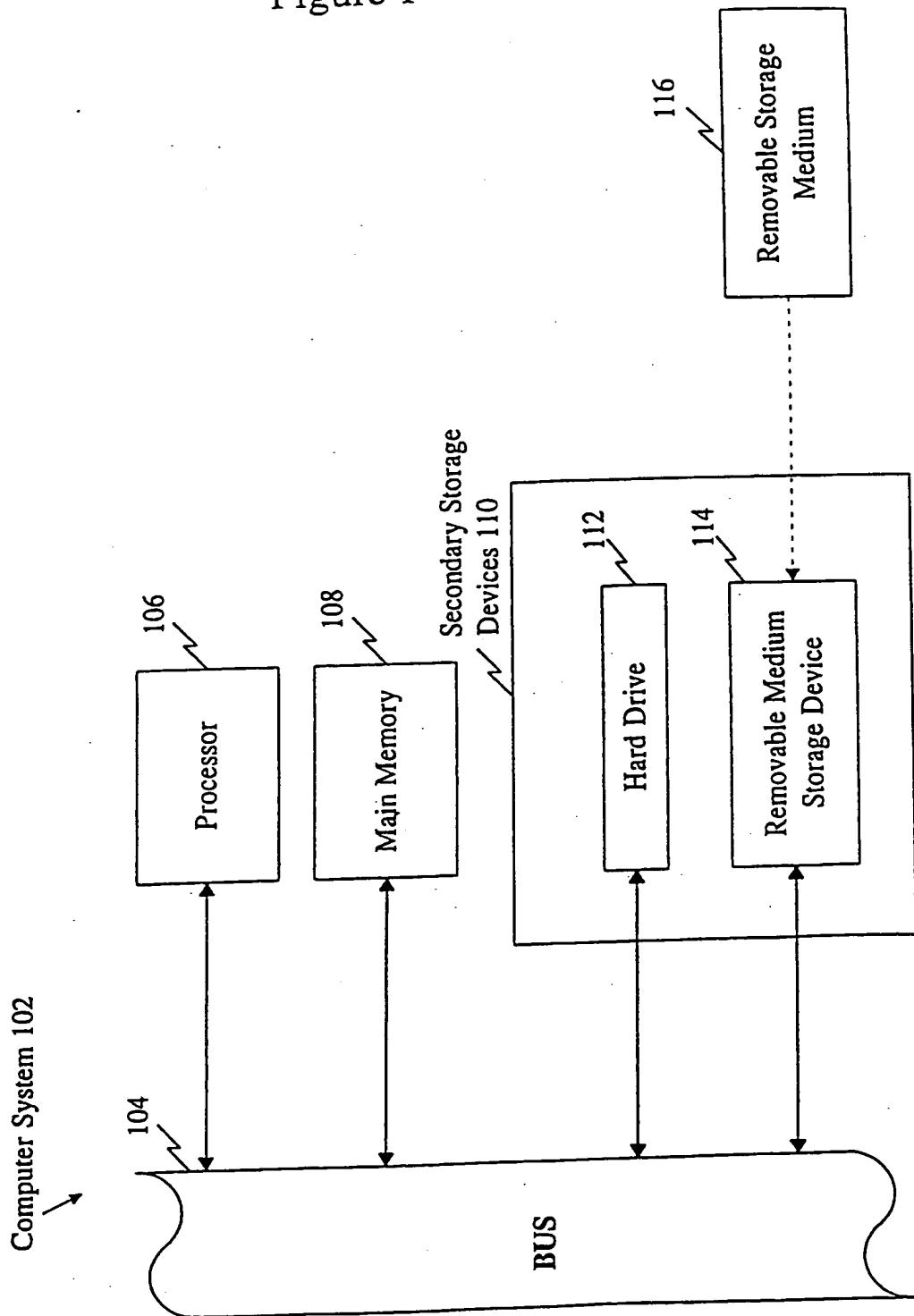


Figure 2

